

GenCore version 5.1.6  
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score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Om nucleic - nucleic search, using sw model  
 Run on: May 18, 2004, 08:59:36 ; Search time 4805 Seconds  
 (without alignments)  
 11/04.115 Million cell updates/sec  
**Title:** US-09-423-410-3  
**Perfect score:** 1231  
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**Scoring table:** IDENTITY\_NUC  
**Gapop:** 10.0 , Gapext: 1.0  
**Searched:** 3470272 seqs, 21671516995 residues  
**Total number of hits satisfying chosen parameters:** 6940544  
**Minimum DB seq length:** 0  
**Maximum DB seq length:** 200000000  
**Post-processing:** Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

**Database :**  
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 29: em\_vii:  
 30: em\_htg\_hum:  
 31: em\_htg\_inv:  
 32: em\_htg\_other:  
 33: em\_htg\_mus:  
 34: em\_htg\_pln:  
 35: em\_htg\_rod:  
 36: em\_htg\_mam:  
 37: em\_htg\_vrt:  
 38: em\_sy:  
 39: em\_htgo\_hum:  
 40: em\_htgo\_mus:  
 41: em\_htgo\_other:

is the number of results predicted by chance to have a

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'2	1231	100.0 ✓	1231 6 AR31140	AR31140 Sequence
'3	1231	100.0 ✓	1231 6 AR399364	AR399364 Sequence
'4	1231	100.0 ✓	1231 6 BD093412	BD093412 Uncouplin
'5	1231	100.0 ✓	1231 9 HAU9763	U84763 Homo sapien
'6	1231	97.7	2340 6 BD106811	AX031190 Sequence
'7	1232	97.7	2340 6 BD106811	BD106811 Human unc
'8	1146.4	93.1	1193 6 A86649	A86649 Sequence 1
'9	1146.4	93.1	1193 6 BD267984	BD267984 Therapeut
'10	1146.4	93.1	1193 6 AX175157	AX175157 Sequence
'11	1146.4	93.1	1193 6 AX31225	AX31225 Sequence
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'15	1100.8	89.4	1104 9 AF011449	AF011449 Homo sapi
'16	981.4	79.7	1132 6 A83295	A83295 Sequence 5
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'19	981.4	79.7	1132 6 AR399365	AR399365 Sequence
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'24	934.4	75.9	936 6 AX103786	AX103786 Sequence
'25	873.8	71.0	1367 4 AF092048	AF092048 Bos tauru
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'27	764.6	62.1	936 4 AB022020	AB022020 Canis fam
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'37	708.8	57.6	1299 10 RNU92069	U92069 Rattus norvegicus
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'42	698.2	56.7	950 10 AF030163	AF030163 Rattus no
'43	695.2	56.6	979 10 AF030164	AF030164 Mus muscu
'44	688.6	55.9	927 10 AB006614	AB006614 Rattus no
'45	680.8	55.3	943 10 AY326457	AY326457 Dicrostonyx

## ALIGNMENTS

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 A83293 A83293  
 LOCUS Sequence 3 from Patent WO9850542.  
 DEFINITION  
 ACCESSION A83293  
 VERSION A83293.1 GI:6732711  
 KEYWORDS  
 SOURCE unidentified  
 ORGANISM unclassified.  
 1 (bases 1 to 1231)  
 Giacobino, J. and Boes, O. / / /  
 UNCOUPLING PROTEIN HOMOLOGUE: UCP 3  
 TITLE  
 PATENT: WO 9850542-A 3 12-NOV-1998;  
 NOVATIS ERFINDUNGEN VERWALTUNG (ATU): GIACOBINO JEAN PAUL (CH)

**FEATURES**

<b>source</b>	Location/Qualifiers
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1. . -1231

/organism="unidentified"  
/molecule\_type="unassigned DNA"  
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Matches 1231; Conservative	0;	Indels 0;
	Gaps 0;	

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121 CCCTAAAGGGACTGAGCACGCTTCAGGACTATGGTGGCTGAGCTGAGCC 180  
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661 CGCAGGGAGGAGGCTGGAGGAATTAACGGGGACTATGGACGCCATAGAACATC 720  
661 CGCAGGGAGGAGGCTGGAGGAATTAACGGGGACTATGGACGCCATAGAACATC 720  
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721 GCTATGCTCACTGTCGAGGGTGGACCTTGACATCTCAAGGAGACTGTCGAC 780  
781 TACACCTGCTCATGACAACGTCCTGGACACTTGCTCTCCCTTGAGCCGCTC 840  
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841 TGTGCGACAGTGGCTCCCGGTTGAGACCGGGTATAGTACTGCT 900  
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901 CCAGGCCAGTACTTCAGGCCCTGACTGTATAGATGGCCAGGGCCCC 960

**RESULT 2**

X AR381440 AR381440 AR381440 Sequence 1 from patent US 6608038. linear PAT 18-DEC-2003

**DEFINITION**

**ACCESSION**

AR381440 AR381440 AR381440 GI:40089474

**VERSION**

.

**KEYWORDS**

.

**SOURCE**

Unknown.

**REFERENCE**

1 (bases 1 to 1231)  
Caplan, S.L., Boettcher, B.R., Slosberg, B.D., Connally, S., Kaleko, M.  
and Derau, U.J.

**AUTHORS**

Methods and compositions for treatment of diabetes and related  
conditions via gene therapy

**TITLE**

Patent: US 6608038-A 1 19-AUG-2003;

**JOURNAL**

**FEATURES**

1. . -1231

/organism="unknown"  
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**ORIGIN**

Query Match	100.0%; Score 1231; DB 6;	Length 1231;
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Matches 1231; Conservative	0;	Indels 0;
	Gaps 0;	

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301 GTCAGAGGGCGCTGGCTGGCTGGAGCTGGCTGGAGCTGGCTGGAGCTGG 360



Qy	901	CCAGGGCGAGTACCTCCACCCCCCTGAGCTGTGATTAAGATGCTGGCCAGGGGCC	960	Db
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Qy	961	ACAGCCTCTACAGGGATTACACCTCTTGCCTTGAGATCTGGAACTGGTG	1020	Db
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Qy	1021	ATGTCCTAACCTATGAGCAGCTGAACGGCCCTGAGTGTAGATAGATGCTGGCCAGGGGCC	1080	Db
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Qy	1081	TGACCGTTTGTGAAACAAGAAGAAGGCACTGTGAGCTAACGTCAGTGTGAAACCGTAG	1140	Db
Db	1081	TGACCGTTTGTGAAACAAGAAGAAGGCACTGTGAGCTAACGTCAGTGTGAAACCGTAG	1140	Qy
Qy	1141	AATGGAGAAAGCGTCACTGAGCACCTCTCTCTTGAGACTCCCTCTCG	1200	Db
Db	1141	AATGGAGAAAGCGTCACTGAGCACCTCTCTTGAGACTCCCTCTCG	1200	Qy
Qy	1141	ATGGAGAAAGCGTCACTGAGCACCTCTCTTGAGACTCCCTCTCG	1200	Db
Db	1141	ATGGAGAAAGCGTCACTGAGCACCTCTCTTGAGACTCCCTCTCG	1200	Qy
Qy	1201	CCTGTTTACTGTGATTCAGAAC	1231	Db
Db	1201	CCTGTTTACTGTGATTCAGAAC	1231	Qy
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DEFINITION	Uncoupling protein homologue: UCP3.			Qy
ACCESSION	BD093412			Db
VERSION	BD093412.1			Qy
KEYWORDS	JP 200152638-A/3.			Db
ORGANISM	Synthetic construct			Qy
REFERENCE	1 (bases 1 to 1231) Giacobino,J.P., MUZZIN,P. and BOSS,O. - / / .			Db
AUTHORS	Giacobino,J.P., MUZZIN,P. and BOSS,O. - / / .			Qy
TITLE	Uncoupling protein homologue: UCP3			Db
JOURNAL	NOVARTIS AG			Qy
COMMENT	JP 200152638-A/3			Db
PP	05-MAY-1998 JP 1998541730			Qy
PR	07-MAY-1997 CH 1072197			Db
PI	JEAN PAUL GIACOBINO, PATRICK MUZZIN, OLIVIER BOSS PC			Qy
C12N15/12, C07K4/705, C12N1/21, A61K4/00, C12N15/86, A61K31/70 CC				Db
Strandedness: Single;				Qy
Topology: Linear;				Db
FH	Key	Location/Qualifiers	Location/Qualifiers	
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Qy	181	CCTCTAACGGACTSGCAGACGCTTGAGTCTGGGCGAGGACAGAGCGCTG	240	Db
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Qy	301	GTCTGAGACGCCGCTCTGAGCTACCTGGCTGGCTGCGACATCCGACCTGG	360	Db
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Qy	421	AGCTTGGCTCATCGACATGGCTCTATACCTCGCTGAGCAGGTGAAACCCCAA	480	Db
Db	481	GCCCGGGACACTCAGCTTACCGGATTGGCCGCTGACCACGGACATG	540	Qy
Qy	481	GCCCGGGACACTCAGCTTACCGGATTGGCCGCTGACCACGGACATG	540	Db
Db	541	GGGGTACCTTGCCAGCCAGAAGTGTGAGGTCCATTAGGGAGCATAC	600	Qy
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Db	661	GGCAGGGAGGAGGAGGTAGGGCTGGGGCTGTGAAAGGAACTTGGCCACATATGAGGAAT	720	Qy
Qy	661	GGCAGGGAGGAGGAGGTAGGGCTGGGGCTGTGAAAGGAACTTGGCCACATATGAGGAAT	720	Db
Db	721	GCTATGTCACAGTGTGAGCTGAGCTGAGGAGCTGAGGAGCTGCTGAGAC	780	Qy
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Db	781	TACCACTGCTGAGCTGAGCAACTTCCCTGCACTTGTGCTCTGCTTGGGCGCTC	840	Qy
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Qy	901	OCAGGGAGTACTCAGCCCTCTGACTGTGAGTAAAGATGTTGGCCAGGGCCC	960	Db
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Qy	961	ACAGCCTTCTACAGGGATTACACCTCTCTGAGTGTGAGTCAGATGTTGGAA	1020	Db
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Db	1081	TGACCGTTTGTGAAACAAGAAGAAGGCACTGTGAGCTAACGTCAGTGTGAAACCGTAG	1140	Qy
Qy	1141	AATGGAGAAAGCGTCACTGAGCACATGGACAGACGCCAGATGTTACAGAA	1200	Db
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ACCESSION	U84763					Db	421 AGCTTGCCTCATCGCATGGCTCTATGACTCGTCAGCAGGTGTAACCCCAA 480
VERSION	U84763.1					Db	481 GCGGGGAACTCCACCTCACTACCGGATTGGCGGTGACCCAGGAGCATG 540
KEYWORDS	Homo sapiens					Db	481 GCGGGGAACTCCACCTCACTACCGGATTGGCGGTGACCCAGGAGCATG 540
SOURCE	(human)					Db	541 GCGGTGACTGTCGCCAGCCACAGATGGTGGGAAGGTTCCGAATTAGGCCAGCATAC 600
ORGANISM	Homo sapiens					Db	541 GCGGTGACTGTCGCCAGCCACAGATGGTGGGAAGGTTCCGAATTAGGCCAGCATAC 600
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. (1 bases 1 to 1231)						Db	601 CTCGGGACATCCAGGAGCAGAACATGGTGAGGGACTATGACCCATAGGCCAGCATAC 660
REFERENCE	Severini, J., Muzzin, P. and Giacobino, J.P. (1997) Uncoupling protein-3: a new member of the mitochondrial carrier family with tissue-specific expression. FEBS Lett. 408 (1), 39-42 (1997)					Db	601 CTCGGGACATCCAGGAGCAGAACATGGTGAGGGACTATGACCCATAGGCCAGCATAC 660
AUTHORS	Boss, O., Samec, S., Paoloni-Giacobino, A., Rossier, C., Dulloo, A., Bos, O., Samec, S., Paoloni-Giacobino, A., Rossier, C., Dulloo, A., (1 bases 1 to 1231)					Db	601 CTCGGGACATCCAGGAGCAGAACATGGTGAGGGACTATGACCCATAGGCCAGCATAC 660
JOURNAL	FEBS Lett. 408 (1), 39-42 (1997)					Db	661 GCGAGGGAGGAGGAGGAGTCAGGGCTGGAGAGAACCTACAGAACCTAC 720
MEDLINE	9724095					Db	661 GCGAGGGAGGAGGAGGAGTCAGGGCTGGAGAGAACCTACAGAACCTAC 720
PUBMED	918264					Db	721 GCTATCGTCAACTGTGTGAGGTGGACTACAGACCTCTGAGGAGGTCTGGAC 780
REFERENCE	2 (bases 1 to 1231)					Db	721 GCTATCGTCAACTGTGTGAGGTGGACTACAGACCTCTGAGGAGGTCTGGAC 780
AUTHORS	Boss, O., Samec, S., Muzzin, P., Rossier, C. and Giacobino, J.-P. (1 bases 1 to 1231)					Db	781 TACCACTGCTACTGACAACTTCCCCTGCACTTGTGCTCTCTGCTTGGACCGGCTTC 840
TITLE	Direct Submission (11-JAN-1997)					Db	841 TGTGCCACAGCTGGACCCGGCGTGGAGAAGGAACTTCCCACATGAGGAT 900
JOURNAL	Medical Biochemistry, Faculty of Medicine, University of Geneva, 1 Michel Servet, Geneva 4, GE 1211, Switzerland					Db	841 TGTGCCACAGCTGGACCCGGCGTGGAGAAGGAACTTCCCACATGAGGAT 900
FEATURES	source					Db	841 TGTGCCACAGCTGGACCCGGCGTGGAGAAGGAACTTCCCACATGAGGAT 900
CDS						Db	841 TGTGCCACAGCTGGACCCGGCGTGGAGAAGGAACTTCCCACATGAGGAT 900
ORIGIN						Db	901 CCGGGCGTGTACTCTAGCCCCCTGAGCTGTATGATAAGATGGTGGCCAGGGGCC 960
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Matches	1231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					Db	961 ACGCTTCTACAGGAACTTACACCTCTTTCGACTGTATGATAAGATGGTGGCCAGGGCCC 1020
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Dy	61 CTCACCGCTGCACTGAAGCCAGGCTGTGGAGCTGGACCTCTCTGGACTCTCTGG 120					Db	1081 TCACCGTTTGACACAAGCAAGAGGACACTGGTAGTAACTGTGTCGAAACCGAGTAA 1140
QY	121 CCTTAAGGGACTGGGAGCACACAAGCTGGCTGGAGCTGGACCTCTGGACTCTGG 180					Db	1081 TCACCGTTTGACACAAGCAAGAGGACACTGGTAGTAACTGTGTCGAAACCGAGTAA 1140
Dy	121 CCTTAAGGGACTGGGAGCACACAAGCTGGCTGGAGCTGGACCTCTGGACTCTGG 180					Db	1141 AATGGAAAAGGGCTACAGCAGAACATGGACAGGACACATGTTACAGAA 1200
QY	181 CCTGCCACCATGGCTGAGGTCGGGAGCACAGGCTGGCTGGACTCTGGACTCTGG 240					Db	1141 AATGGAAAAGGGCTACAGCAGAACATGGACAGGACACATGTTACAGAA 1200
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QY	241 GTTACCTTCCCTGGACACACAAGCTCCCTGCGATCGAGGAGGACATCTGACCTGG 300					Db	1201 CTGTGTTACTGTGCTGATCAAGAAC 1231
Dy	241 GTTACCTTCCCTGGACACACAAGCTCCCTGCGATCGAGGAGGACATCTGACCTGG 300					Db	301 GTCGAGCGCCCGCTGCTGGAGTACGGTGGCTGGACCTCTGACCTGG 360
QY	301 GTCGAGCGCCCGCTGCTGGAGTACGGTGGCTGGACCTCTGACCTGG 360					Db	301 GTCGAGCGCCCGCTGCTGGAGTACGGTGGCTGGACCTCTGACCTGG 360
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DEFINITION	Sequence 11 from Patent WO9852958.						
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VERSION	AX031190.1						
KEYWORD	unidentified						
SOURCE	unidentified						
ORGANISM	unclassified						
REFERENCE	1						
AUTHORS	Chen, F. and Liu, Q.						

TITLE	Human uncoupling protein 3
JOURNAL	
PATENT:	WO 9852950-A 11 26-NOV-1998;
CHEN FANG (US) ; LIU QINGXUN (US) ; MERCK & CO INC (US)	
FEATURES	
Source	1. . 2340 /mol_type="unassigned DNA" /db_xref="taxon:32644"
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Query Match	97.7%; Score 1202.2; DB 6; Length 2340;
Best Local Similarity	99.6%; Pred. No. 8.2e-250;
Matches	1226; Conservative 0; Mismatches 3; Indels 2; Gaps 2;
Qy	1 TCTCTGGATGAGCCCTAGGGAGCCCTGTGCTGCCTGAGCTTGACGCC 60
Db	193 TCTCTGGATGAGCCCTAGGGAGCCCTGTGCTGCCTGAGCTTGACGCC 252
Qy	61 CCACCGCTGCTGAGGCCCTAGGGAGCCCTGTGCTGCCTGAGCTTGACGCC 60
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Qy	121 CCTTAAGGACTGGGAGAGCCTCAGGACTATGGTCACTGAGCTTCAGCTG 180
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Qy	181 CTCCTCCACCATGGCTGAGCTTCCTGGGGAGGGAGCTGCTGAGCTC 240
Db	371 CTCCTCCACCATGGCTGAGCTTCCTGGGGAGGGAGCTGCTGAGCTC 430
Qy	241 GTTACCTTCCTGACACGCCAACGTCGCCCTGAGTCAGGGAGAACGGCG 300
Db	431 GTTACCTTCCTGACTGAGCCACACGCCAACGTCGCCCTGAGTCAGGGCG 490
Qy	301 GTTACCTTCCTGACTGAGCCACACGCCAACGTCGCCCTGAGTCAGGGCG 360
Db	491 GTTACCTTCCTGACTGAGCCACACGCCAACGTCGCCCTGAGTCAGGGCG 550
Qy	361 CGACTCTGGGCTCTGAGCCCTACATGGCTGGGGGGCTGAGCCAGATG 420
Db	551 CGACTCTGGGCTCTGAGCCCTACATGGCTGGGGGGCTGAGCCAGATG 610
Qy	421 AGCTTCCTCCATGCCATGCCCTATGACTCTGAGCTGGTACCCCCAA 480
Db	611 AGCTTCCTCCATGCCATGCCCTATGACTCTGAGCTGGTACCCCCAA 670
Qy	481 GGGGGGAACACTCCAGCTCACTACCGGATTGGCGCGCTGACACAGGGATG 540
Db	671 GGGGGGAACACTCCAGCTCACTACCGGATTGGCGCGCTGACACAGGGATG 730
Qy	541 GGGGTGACTCTGGCCAGCCACAGATGTGAGGTGGTGGAGGCTGATG 600
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Query Match	97.7%; Score 1202.2; DB 6; Length 2340;
Best Local Similarity	99.6%; Pred. No. 8.2e-250;
Matches	1226; Conservative 0; Mismatches 3; Indels 2; Gaps 2;
Qy	1 TCTCTGGATGAGCCCTAGGGAGCCCTGTGCTGCCTGAGCTTGACGCC 60
Db	193 TCTCTGGATGAGCCCTAGGGAGCCCTGTGCTGCCTGAGCTTGACGCC 252
Qy	61 CCACCGCTGCTGAGGCCCTAGGGAGCCCTGTGCTGCCTGAGCTTGACGCC 60
Db	253 CCACCGCTGCTGAGGCCCTAGGGAGCCCTGTGCTGCCTGAGCTTGACGCC 310
Qy	121 CCTTAAGGACTGGGAGAGCCTCAGGACTATGGTCACTGAGCTTCAGCTG 180
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LOCUS	BD106811
DEFINITION	Human uncoupling protein 3.
ACCESSION	BD106811
VERSION	BD106811.1 GI:23201629
KEYWORDS	JP 200202240-A/11.
SOURCE	Mus musculus (house mouse)
ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuropipathi; Muridae; Murinae; Mus.
REFERENCE	(bases 1 to 2340)
AUTHORS	Liu, Q. and Chen, F.
TITLE	Human uncoupling protein 3
JOURNAL	Patent: JP 200202240-A 11 22-JAN-2002;
COMMENT	MERCK & CO INC
PD	PN JP 200202240-A/11
PR	22-JAN-2002
PP	19-MAR-1998 JP 1998550522
PR	20-MAY-1997 US 60/057179, 08-AUG-1997 GB 9716886.8 PR
PI	QINGXUN LIU, FANG CHEN
PC	C09H7/00, C12B21/06, C12N1/20, C12N15/00
CC	Strandedness: Double;
CC	Topology: Linear;
FH	Key Location/Qualifiers
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 QY 301 GTCAGAGGGCGGGCGGTGAGTACGGTGGGGCGTGCAGATCAGGGGAGACGG 360  
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 QY 481 GCGCGGAGAACCTCAGGCTCTACCGGATTGGCGGGTGACACAGGTTACACCCCAA 540  
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 QY 541 GCGGTGACCTGGCCAGCCCCAGATGGAGGTGGATCAGGGCGATCAC 600  
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 QY 1141 ATGGAGAACAGGGTGTGAAAGGGGCTGTGAAAGTCCAGATGTTACSGAA 1200  
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**RESULT 8**  
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 ACCESSION A86649 VERSION A86649.1 GI:6735204  
 KEYWORDS SOURCE unidentified  
 ORGANISM unidentified  
 REFERENCE unclassified.  
 AUTHORS Godden, R. J. and Paine, K.  
 TITLE POLYNUCLEOTIDES AND POLYPEPTIDES BELONGING TO THE UNCOUPLING PROTEINS FAMILY  
 JOURNAL Patent: WO 9339432-A 1 11-SEP-1998;  
 GODDEN, ROBERT JAMES (GB); PAYNE, KELLY (GB)  
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**ORIGIN**

Query Match<sup>h</sup> 93.1%; score 1146; DB: 6; Length: 1193;  
 Best Local Similarity 99.9%; Pred. No. 1e-237; Mismatches 0; Indels 0; Gap 0;

Matches 1147; Conservative 0; MisMatches 1; Indels 0; Gap 0;  
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 QY 61 CCACCGCTGCACTGAAGCCAGGGCTGGAGCCTCTCTGGAGACCTCTCTGGCGCTGCGAGGACTCACGGC 120  
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 QY 121 CCTTAAGGGACTGGGAGGCTCTGGAGGACTATGTTGGACTGTGAGGCTTCAGAGTG 180  
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 QY 181 CCTCCACCATGGCTGAGTGGTCTGGGAGGGCTCAGGCGCTCAGGCGCTTCTGG 240  
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 QY 241 GTTACCTTCACTGAAACAGCCAGGGCTGGAGATCAGGGAGAACCGGG 300  
 Db 286 GTTACCTTCACTGAAACAGCCAGGGCTGGAGATCAGGGAGAACCGGG 345  
 QY 301 GTCAGAGGGCCGGCTGGTGTGAGCTGGCTGGAGGCTGGAGGCTGG 360  
 Db 346 GTCAGAGGGCCGGCTGGTGTGAGCTGGCTGGAGGCTGGAGGCTGG 405  
 QY 361 CGGACTGGGGCTGGAGCCCTACATGGCTGTGGGGCTCAGGCCAGTG 420  
 Db 406 CGGACTGGGGCTGGAGCCCTACATGGCTGTGGGGCTCAGGCCAGTG 465  
 QY 421 AGTTGCGCTCATCCGGATCGCCCTATGACTCCGGTCAAGGGAGTGG 480  
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 QY 481 GCGGGAGAACCTGGCTACTACGGGATTGGCGCTGACCAAGGAGCTG 540  
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 QY 601 CTGGGGCATCCAGGAGGACGAAATACAGGGGACTATGAGCCCTACAGAACCTC 660  
 Db 646 CTGGGGCATCCAGGAGGACGAAATACAGGGGACTATGAGCCCTACAGAACCTC 705





Qy	1	TCTTGGGATGGGCCCTGGAGGCCCTGGCTGCGCTGGCAGGACTCAAGCC	60	Db	1081 TACCGTTTGACAGACAGAAGGCCACTGTGACTAAGTGTGCGAAGCAGTAG	1140
Qy	46	TCTGGGATGGGCCCTGGCTGCGCTGGCAGGACTCAAGCC	105	Db	1126 TACCGTTTGACAGACAGAAGGCCACTGTGACTAAGTGTGCGAAGCAGTAG	1185
Qy	61	CCACCGTGCACAGAACGCCCTGGCTGCGCTGGCAGGACTCAAGCC	120	Db	1141 ATGGAAAG 1148	
Qy	106	CCACCGTGCACAGAACGCCCTGGCTGCGCTGGCAGGACTCAAGCC	165	Db	1186 AATGGAAG 1193	
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Qy	166	CCCTAAAGGGACTGGCAGAGCCTCCGGACTATGGTGAATGAGCTTCAGGCTG	225	Db	BD178217	
Qy	181	CCTCCACCATGGCTGAGATTCCTGGGGCAAGCACAGCAGCTGTTGTAACCT	240	Db	BD178217	
Qy	226	CCTCCACCATGGCTGAGATTCCTGGGGCAAGCACAGCAGCTGTTGTAACCT	285	Db	BD178217.1 GT:30015481	
Qy	241	GTACTTTCACAGACAGAACGCCCTGGCTGCGCTGGCAGGACTCAAGCC	300	Db	JP 2002300891-A/1.	
Qy	286	GTACTTTCACAGACAGAACGCCCTGGCTGCGCTGGCAGGACTCAAGCC	345	Db	Patent: JP 2002300891-A 1 15-OCT-2002;	
Qy	301	GTCCGACAGGCCCGCTCGCACTACCGTGGGTGCTGGGACCCATCTGACATG	360	Db	SMITHKLINE BEPHAM PLC	
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Qy	481	GCGCGGACAACCTCAGCTCACTACCGGATTGGCGGTGCAACACAGGCGATG	540	Db	PI LEE JAMES BEELEY, KELLY Paine ROBERT JAMES GODDEN PC	
Qy	526	GCGCGGACAACCTCAGCTCACTACCGGATTGGCGGTGCAACACAGGCGATG	585	Db	C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10,	
Qy	541	GCGGAGCTGTGCCAGGCCACAGGAGCAAGAAATACAGCGGACTATGGACGCCATAC	600	Db	PC A61P3/04, C12P21/02, C12Q1/02, C12Q1/68, G01N33/15, G01N33/50/A61K45/00, PC	
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Qy	946	CCAGCGCACTGCTGCTCCCTGGAGGTGGAGAACCCCTATATGACTCACCT	1005	Db	Matches 1147; Conservativeness 0; Mismatches 1; Indels 0; Gaps 0;	
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Qy	501 CTGGGAACTCTGGCCAGGCCAACAGATGGTGAAGGCTGGCTGACGGGACATC 600		
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Qy	721 GCTATCTCAACTGTGCTGAGGGACTAACCTCTGGCTGAGCTTGGAC 780		
Db	766 GCTATCTCAACTGTGCTGAGGGACTAACCTCTGGAC 825		
Qy	781 TACCACTGCTACTGACAACTTGGCTGAGCTTGGAC 840		
Db	826 TACCACTGCTACTGACAACTTGGCTGAGCTTGGAC 885		
Qy	841 TGTGCCAGTAGGGCTCCCGGTGAGCTGGTGAAGACCGGTATGACTCCT 900		
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Db	1186 ATGGAAAG 1193		
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REFERENCE Beeley, J., James, Paine, K. and Godden, R. James. AUTHORS Polypeptides and polypeptides belonging to the uncoupling proteins family			



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 ACCESSION AF011449  
 VERSION AF011449.1 GI:2440012  
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 ORGANISM Homo sapiens  
 AUTHORS 1. (bases 1 to 1104)  
 TITLE Uncoupling protein-3 is a mediator of thermogenesis regulated by  
 JOURNAL thyroid hormone, beta<sub>3</sub>-adrenergic agonists, and leptin  
 MEDLINE 97450925  
 PUBMED 9105858  
 REFERENCE 2. (bases 1 to 1104)  
 AUTHORS Gong, D.-W., He, Y., Karas, M. and Reitman, M.  
 TITLE Direct Submission  
 JOURNAL Submitted (30-JUN-1997) Diabetes Branch, NIDDK/NIH, Bldg 10/Rm  
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ORIGIN

Query Match Score 1100.8; DB 9; Length 1104;  
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QY 176 AGTGCCTCCGCCATGGCTGGAGTTCTGGGAGGGCTGGACAGCCCTCTTGACCTCT 235  
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QY 236 ACTCTGTTACCTTCCACTGAGCACGCCAGAGTCCAGATTCAGGGAGACC 295  
 Db 181 ACTCTGTTACCTTCCACTGAGCACGCCAGAGTCCAGATTCAGGGAGACC 240

QY 296 AGGGGGTCCAGAGGGGGGGCTGGAGTGGAGGTTGGGACCCATTCTGACCA 355  
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QY 356 TGGTGCAGTAGGGGAGCCCTGAGCCCTAAATGGCTGGGGGGCTGGAGGCC 415  
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 Db 361 AGATAGCTTGCCCTCCATCGCATCGGCCCTATGACTCGTCAGAGGTGACCC 420

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QY 536 CCATGAGGAGACTCTGCCAGCCACAGAGTGGTCAATTAGGGCAGCA 595  
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QY 596 TACACCTGGSCCATCCAGAGGAGCAGAAATACGGGAACTATGGACCTACAGAA 655  
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QY 836 GCTTCCTGCCACAGTGTGCTCCGGTGGACCTGTCAGAAGCAGCCGGTATGACT 895  
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QY 956 GCCCCACGCCCTCTGAGGGATTACACCTCCCTTTCGTTGGATCCTGGACCG 1015  
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QY 1016 TGGTGTGTTGAACTTATGAGACCTGAGCCCTGAGAAGTCCAGATGTCAC 1075  
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QY 1136 TTAAGATGGAGAACGGTCA 1159 ---  
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GenCore version 5.1.6  
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Om nucleic - nucleic search, using sw model

Run on: May 18, 2004, 11:12:25 ; Search time 123 Seconds

(without alignments) 5554.021 Million cell updates/sec

Title: US-09-423-410-3

Perfect score: 1231  
 Sequence: tcctggatggaggccctagg.....ttgttgattcaagaaac 1231

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 2747546 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:\*

1: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq: \*  
 2: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq: \*  
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 4: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq: \*  
 5: /cgn2\_6/ptodata/2/ina/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	1231	100.0	1231	4	US-09-423-410-3	Sequence 1, Appli
2	1231	100.0	1231	4	US-09-423-410-3	Sequence 3, Appli
3	1145.4	93.0	1192	3	US-09-142-565-1	Sequence 1, Appli
4	981.4	79.7	1132	4	US-09-808-457-3	Sequence 3, Appli
5	981.4	79.7	1132	4	US-09-423-410-5	Sequence 5, Appli
6	732	59.5	2782	2	US-09-937-466-1	Sequence 1, Appli
7	732	59.5	2782	3	US-09-172-528-1	Sequence 1, Appli
8	732	59.5	2782	3	US-09-318-199-1	Sequence 1, Appli
9	732	59.5	2782	3	US-09-503-579-1	Sequence 1, Appli
10	705.4	57.3	1949	2	US-09-937-466-3	Sequence 3, Appli
11	705.4	57.3	1949	2	US-09-172-528-3	Sequence 1, Appli
12	705.4	57.3	1949	3	US-09-318-199-3	Sequence 1, Appli
13	705.4	57.3	1949	3	US-09-503-579-3	Sequence 1, Appli
14	593.8	48.2	1777	2	US-08-937-466-5	Sequence 1, Appli
15	593.8	48.2	1777	2	US-09-172-528-5	Sequence 3, Appli
16	593.8	48.2	1777	3	US-09-318-199-5	Sequence 5, Appli
17	593.8	48.2	1777	3	US-09-503-579-5	Sequence 5, Appli
18	476.6	38.7	1596	2	US-08-807-868A-38	Sequence 3, Appli
19	476.6	38.7	1596	3	US-09-210-681-38	Sequence 3, Appli
20	476.6	38.7	1596	3	US-08-946-719A-38	Sequence 3, Appli
21	476.6	38.7	1596	4	US-09-541-983-38	Sequence 3, Appli
22	475.6	38.6	930	4	US-0-001-0511-1	Sequence 1, Appli
23	457.2	37.1	1255	1	US-08-518-878B-38	Sequence 3, Appli
24	457.2	37.1	1255	1	US-08-291-522B-38	Sequence 3, Appli
25	457.2	37.1	1255	2	US-08-470-868A-38	Sequence 3, Appli
26	441.8	35.9	847	3	US-08-142-565-5	Sequence 5, Appli
27	385.6	31.3	1205	1	US-08-294-522B-37	Sequence 37, Appli
28	385.6	31.3	1205	2	US-08-807-661A-36	Sequence 36, Appli
29	385.6	31.3	1205	3	US-08-470-868A-36	Sequence 36, Appli
30	385.6	31.3	1205	3	US-09-210-681-36	Sequence 36, Appli
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33	385.6	31.3	1205	4	US-09-023-659-890	Sequence 890, Appli
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36	254.4	20.7	512	4	US-09-735-457-1014	Sequence 1014, APPL
37	254.4	20.7	512	4	US-09-614-14B-1014	Sequence 1014, APPL
38	254.4	20.7	512	4	US-09-671-525-1014	Sequence 1014, APPL
39	201	16.3	222	3	US-09-142-555-3	Sequence 3, Appli
40	171.6	13.9	309	1	US-08-518-878B-14	Sequence 14, Appli
41	171.6	13.9	309	1	US-08-294-522B-14	Sequence 14, Appli
42	171.6	13.9	309	2	US-08-807-861A-14	Sequence 14, Appli
43	171.6	13.9	309	2	US-08-470-868A-14	Sequence 14, Appli
44	171.6	13.9	309	3	US-09-210-681-14	Sequence 14, Appli
45	171.6	13.9	309	3	US-08-946-719A-14	Sequence 14, Appli

#### ALIGNMENTS

##### RESULT 1

US-09-808-457-1

Sequence 1, Application US/09808457  
 Patent No. 6608038

GENERAL INFORMATION:  
 APPLICANT: Boettcher, Brian  
 APPLICANT: Caplan, Shari  
 APPLICANT: Kaleko, Michael  
 APPLICANT: Connely, Sheila  
 APPLICANT: Desai, Urvi  
 APPLICANT: Slosberg, Eric  
 TITLE OF INVENTION: Methods and Compositions For Treatment  
 TITLE OF INVENTION: of Diabetes and Related Conditions Via Gene Therapy  
 FILE REFERENCE: 4-3133A/USN  
 CURRENT APPLICATION NUMBER: US/09/808 457  
 CURRENT FILING DATE: 2001-03-14  
 PRIOR APPLICATION NUMBER: 60/XXX,XXX  
 PRIOR FILING DATE: 2000-03-15  
 NUMBER OF SEQ ID NOS: 10  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 1  
 LENGTH: 1231  
 TYPE: DNA  
 ORGANISM: Unknown  
 FEATURE: 100.0%; Score 1231; DB 4; Length 1231;  
 OTHER INFORMATION: cDNA from clone UCP3L

US-09-808-457-1

Query Match 100.0%; Score 1231; DB 4; Length 1231;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-307;  
 Matches 1231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3  
US-09-142-565-1  
; Sequence 1, Application US/09142565A.  
; Patent No. 6185560  
; GENERAL INFORMATION:  
; APPLICANT: Kelly Paine  
; APPLICANT: Robert James B  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GH-3-0002  
; CURRENT APPLICATION NUMBER: US/09/142,565A  
; CURRENT FILING DATE: 1999-06-30  
; EARLIER APPLICATION NUMBER: 9704551.2  
; EARLIER FILING DATE: 1997-03-05  
; EARLIER APPLICATION NUMBER: 9705614.7  
; EARLIER FILING DATE: 1997-03-18  
; EARLIER APPLICATION NUMBER: 97303305.1  
; EARLIER FILING DATE: 1997-07-16  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 1192  
; TYPE: DNA  
; ORGANISM: HOMO SAPIEN  
; US-09-142-565-1

Query Match 93.0%; Score 1145.4; DB 3; Length 1192;  
Best Local Similarity 99.9%; Pred. No. 2.9e-285; Mismatches 1; Indels 0; Gaps 0;  
Matches 1146; Conservative 0;

QY 1 TCTCTGGATGAGGCCCTAGGAGCCCTTGCTGCCCCCTGCTGGCGGACATCACGCC 60  
Db 46 TCCGGGATGAGGCCCTAGGAGCCCTTGCTGCCCCCTGCTGGCGGACATCACGCC 105  
QY 61 CACACGGCTCACTGAGCCGAGGCTGTGAGCAGCTCTCTCTGGACCTCTGG 120

Db 106 CCACCCCTGCACTGAGCCAGGGCTGTGAGCAGCCCTCTCTGGACCTCTGG 165  
QY 121 CCCTAAAGGGACTGCGCAAGGCCTTCAGGACTATGGTGGACTGAGCTTCAGAOGT 180  
Db 166 CCCTAAAGGGACTGCGCAAGGCCTTCAGGACTATGGTGGACTGAGCTTCAGAOGT 225  
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Db 346 GTTACAGGAGGCGGGCTGTGAGCTGAGTGGACCCAGGGGGCCC 405  
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Db 406 CGTACAGGAGGCGGGCTGTGAGCTGAGTGGACCCAGGGGGCCC 465  
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Db 466 AGCTTGCCCTCATCGCCATCGCCCTTACATGGCTGTGAGCTGACCCCAA 525  
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Db 526 GCGCGAGAACCTCCAGCTCACTACCGGATTTCGGCTGACACGGAGCATG 585  
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Db 586 GCGTGAACCTGGCCAGGGACAGATGTTGGTGAAGGTCCATTGGCCAGCATAC 645  
QY 601 CTGGGGCATCAGGGAGCAGAATACGGGACTATGACCCCTACTGAACATC 660  
Db 646 CTGGGGCATCAGGGAGCAGAATACGGGACTATGACCCCTACTGAACATC 705  
QY 661 GCGAGGGAGGAGGACTGGGGCTGTGGAAAGAAACTTCCCAAATCATGAGGAT 720  
Db 706 GCGAGGGAGGAGGACTGGGGCTGTGGAAAGAAACTTCCCAAATCATGAGGAT 765  
QY 721 GCTATCCTCAACTGTGTTGAGGTGGTCACTAGACATCTCAAGGAGGTCTGGAC 780  
Db 766 GCTATCCTCAACTGTGTTGAGGTGGTCACTAGACATCTCAAGGAGGTCTGGAC 825  
QY 781 TACCACTGCTCACTGACAACACTCCCTGCACTAGACATCTCAAGGAGGTCTGGAC 840  
Db 826 TACCACTGCTCACTGACAACACTCCCTGCACTAGACATCTCAAGGAGGTCTGGAC 885  
QY 841 TGTGCCACAGTGTTGGCTCCCGGTTGGAGAAGGACTTGGCCAAATCATGAGGAT 900  
Db 886 TGTGCCACAGTGTTGGCTCCCGGTTGGAGAAGGACTTGGCCAAATCATGAGGAT 945  
QY 901 CTGGCCAGTACTTCAGCCCTTGACTGTGTTGATATAAGATGGTGGCCAGGGCCC 960  
Db 946 CTGGCCAGTACTTCAGCCCTTGACTGTGTTGATATAAGATGGTGGCCAGGGCCC 1005  
QY 961 ACAGCCTCTACAGGATTACCCCTCTTGGTTGGATCTGGACCTGG 1020  
Db 1006 ACAGCCTCTACAGGATTACCCCTCTTGGTTGGATCTGGACCTGG 1065  
QY 1021 ATGTCGTAACCTATGAGCAGTGAAAGGGCTGTGAAGCTTCAAGTGTACGGAA 1080  
Db 1066 ATGTCGTAACCTATGAGCAGTGAAAGGGCTGTGAAGCTTCAAGTGTACGGAA 1125  
QY 1081 TCACTGGTTTGACAGAGCAAGGACCTGTGTTGATCTGGACCTGGCTTCACAGTGTACGGAA 1140  
Db 1126 TCACTGGTTTGACAGAGCAAGGACCTGTGTTGATCTGGACCTGGCTTCACAGTGTACGGAA 1185  
QY 1141 ATGGAA 1147  
Db 1186 ATGGAA 1192

RESULT 4  
US-09-808-457-3  
; Sequence 3, Application US/09808457  
; GENERAL INFORMATION:  
; APPLICANT: Boettcher, Brian  
; APPLICANT: Caplan, Shari  
; APPLICANT: Kajeko, Michael  
; APPLICANT: Connally, Sheila  
; APPLICANT: Deasi, Uri  
; APPLICANT: Sloberg, Eric  
TITLE OF INVENTION: Methods and Compositions For Treatment  
; TITLE OF INVENTION: Of Diabetes and Related Conditions Via Gene Therapy  
FILE REFERENCE: 4-31353A/USN  
CURRENT APPLICATION NUMBER: US/09/808, 457  
CURRENT FILING DATE: 2001-03-14  
PRIORITY APPLICATION NUMBER: 60/XXX, XXX  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 1132  
TYPE: DNA  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: cDNA from clone UCP3S  
US-09-808-457-3

Query Match 79.7%; Score 981 4; DB 4; Length 1132;  
Best Local Similarity 99.4%; Pred. No. 4.5e-243;  
Matches 985; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TCCTGGAGATGAGGCCCTAGGAGGCCCTGTGCTGCCTGGCGTGAAGACCTTGCCACACATCATAGGAT 60  
Db 1 TCCTGGAGATGAGGCCCTAGGAGGCCCTGTGCTGCCTGGCGTGAAGACCTTGCCACACATCATAGGAT 60  
Qy 61 GCACCGCTGCACTGAAAGCCCTGGCGTGAAGACCTTGCCACACATCATAGGAT 60  
Db 61 GCACCGCTGCACTGAAAGCCCTGGCGTGAAGACCTTGCCACACATCATAGGAT 60  
Qy 61 GCACCGCTGCACTGAAAGCCCTGGCGTGAAGACCTTGCCACACATCATAGGAT 60  
Db 61 GCACCGCTGCACTGAAAGCCCTGGCGTGAAGACCTTGCCACACATCATAGGAT 60  
Qy 121 CCTCTAACAGGACTGCGAGACCTTCAGACTATGGTGCAGCTAGCTAACCTCACAGCC 60  
Db 121 CCTCTAACAGGACTGCGAGACCTTCAGACTATGGTGCAGCTAGCTAACCTCACAGCC 60  
Qy 121 CCTCTAACAGGACTGCGAGACCTTCAGACTATGGTGCAGCTAGCTAACCTCACAGCC 60  
Db 121 CCTCTAACAGGACTGCGAGACCTTCAGACTATGGTGCAGCTAGCTAACCTCACAGCC 60  
Qy 181 CCTCCCACCATGGCTGAGGTCTGGGGAGGGACAGGAGCCGTTGGTGCACCTC 120  
Db 181 CCTCCCACCATGGCTGAGGTCTGGGGAGGGACAGGAGCCGTTGGTGCACCTC 120  
Qy 181 CCTCCCACCATGGCTGAGGTCTGGGGAGGGACAGGAGCCGTTGGTGCACCTC 120  
Db 181 CCTCCCACCATGGCTGAGGTCTGGGGAGGGACAGGAGCCGTTGGTGCACCTC 120  
Qy 181 CCTCCCACCATGGCTGAGGTCTGGGGAGGGACAGGAGCCGTTGGTGCACCTC 120  
Db 181 CCTCCCACCATGGCTGAGGTCTGGGGAGGGACAGGAGCCGTTGGTGCACCTC 120  
Qy 241 GTTACCTTCCACTGGACACCAAGGTCCGCTGAGATCCAGGGGAGAACCGGC 180  
Db 241 GTTACCTTCCACTGGACACCAAGGTCCGCTGAGATCCAGGGGAGAACCGGC 180  
Qy 241 GTTACCTTCCACTGGACACCAAGGTCCGCTGAGATCCAGGGGAGAACCGGC 180  
Db 241 GTTACCTTCCACTGGACACCAAGGTCCGCTGAGATCCAGGGGAGAACCGGC 180  
Qy 301 GTCGACAGCGGCCGAGCTGAGTACCGTGACCTGAGCTGGCTACCGATG 360  
Db 301 GTCGACAGCGGCCGAGCTGAGTACCGTGACCTGAGCTGGCTACCGATG 360  
Qy 361 CGACAGCTGGCTCTGGAGGCCCTAGTGGCGCTACCGATG 420  
Db 361 CGACAGCTGGCTCTGGAGGCCCTAGTGGCGCTACCGATG 420  
Qy 421 AGCTTCGCTCCATCCCGATCGCCCTCTATGACTCCCTCAACGGGTAAACCCCAA 480  
Db 421 AGCTTCGCTCCATCCCGATCGCCCTCTATGACTCCCTCAACGGGTAAACCCCAA 480  
Qy 481 GCGCGGCGCAACTCCAGCTTACCCGGATTGGCCGCTGACCGACGACGATG 540  
Db 481 GCGCGGCGCAACTCCAGCTTACCCGGATTGGCCGCTGACCGACGACGATG 540  
Qy 541 GGGTGAACCTGAGCCACAGATGGTGAAGSTCCCAATTTCAGGCGACGACAC 600  
Db 541 GGGTGAACCTGAGCCACAGATGGTGAAGSTCCCAATTTCAGGCGACGACAC 600

RESULT 5  
US 09-423-410-5  
; Sequence 5, Application US/09423410  
; Patent No. 6620594  
; GENERAL INFORMATION:  
; APPLICANT: Giacobino, Jean-Paul  
; APPLICANT: Muzzin, Patrick  
; APPLICANT: Boss, Olivier  
TITLE OF INVENTION: UNCOUPLING PROTEIN HOMOLOGUE: UCP3  
FILE REFERENCE: 4-3053/A  
CURRENT APPLICATION NUMBER: US/09/23, 410  
CURRENT FILING DATE: 1999-11-04  
EARLIER APPLICATION NUMBER: PCT/EP98/02645  
EARLIER FILING DATE: 1998-05-05  
EARLIER APPLICATION NUMBER: 1072/97  
EARLIER FILING DATE: 1997-05-07  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5  
LENGTH: 1132  
TYPE: DNA  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Description of Unknown Organism: cDNA from clone UCP3S  
US-09-423-410-5

Query Match 79.7%; Score 981 4; DB 4; Length 1132;  
Best Local Similarity 99.4%; Pred. No. 4.5e-243;  
Matches 985; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TCCTGGAGATGAGGCCCTAGGAGGCCCTGTGCTGCCTGGCGTGAAGACCTTGCCACACATCATAGGAT 60  
Db 1 TCCTGGAGATGAGGCCCTAGGAGGCCCTGTGCTGCCTGGCGTGAAGACCTTGCCACACATCATAGGAT 60  
Qy 61 CCACCGCTGCACTGAAAGCCCTGGCGTGAAGACCTTGCCACACATCATAGGAT 60  
Db 61 CCACCGCTGCACTGAAAGCCCTGGCGTGAAGACCTTGCCACACATCATAGGAT 60  
Qy 61 CCACCGCTGCACTGAAAGCCCTGGCGTGAAGACCTTGCCACACATCATAGGAT 60  
Db 61 CCACCGCTGCACTGAAAGCCCTGGCGTGAAGACCTTGCCACACATCATAGGAT 60  
Qy 121 CCTCTAACAGGACTGCGAGACCTTCAGACTATGGTGCAGCTAGCTAACCTCACAGCC 120  
Db 121 CCTCTAACAGGACTGCGAGACCTTCAGACTATGGTGCAGCTAGCTAACCTCACAGCC 120  
Qy 121 CCTCTAACAGGACTGCGAGACCTTCAGACTATGGTGCAGCTAGCTAACCTCACAGCC 120  
Db 121 CCTCTAACAGGACTGCGAGACCTTCAGACTATGGTGCAGCTAGCTAACCTCACAGCC 120

Qy 181 CCTCCGACCACTGGCTGAACTTCCTGGGAGGAGGAGGAGCCTGGTGTGACTC 240  
Db 181 CCTCCCACCATGGCTGTGAAGTCTCTGGGGAGGAGGAGCCTGGTGTGACTC 240  
Qy 241 GTTACCTTCCATGGACACAGCCAAAGGTGGCTCGAGTCAGTCAGGGAGGG 300  
Db 241 GTTACCTTCCATGGACACAGCCAAAGGTGGCTCGAGTCAGTCAGGGAGGG 300  
301 GTTCCAGAGGGCGGTGCTGGAGTACCGTGCTGGGCTCTGGAGGAGGAGGG 300  
Db 301 GTTCCAGAGGGCGGTGCTGGAGTACCGTGCTGGGCTCTGGAGGAGGG 300  
361 CGGAGCTGGGCTCTGGAGGCCAATGGCTGTGGGGCTTGAGGGAGGG 420  
Db 361 CGGAGCTGGGCTCTGGAGGCCAATGGCTGTGGGGCTTGAGGGAGGG 420  
Qy 421 AGCTTGCCCTACATGGCTGGCTGAGGCTCAAGCAGGGTGACACCCCAA 480  
Db 421 AGCTTGCCCTACATGGCTGGCTGAGGCTCAAGCAGGGTGACACCCCAA 480  
481 GCGCGGAGAACCTCCAGGCTCTACCGGATTGGCGGCTGACACGGGAGGG 420  
Qy 481 GCGCGGAGAACCTCCAGGCTCTACCGGATTGGCGGCTGACACGGGAGGG 420  
Db 481 GCGCGGAGAACCTCCAGGCTCTACCGGATTGGCGGCTGACACGGGAGGG 540  
Qy 541 GCGGTGACTCTGGCCAGGCCAGATGGTGAAGSTCCGTTAGGCAGCATAC 600  
Db 541 GCGGTGACTCTGGCCAGGCCAGATGGTGAAGSTCCGTTAGGCAGCATAC 600  
Qy 601 CTGGGSCCATCTGGAGGAGCAGAAATACTACGGGACTATGGACGCTAC 660  
Db 601 CTGGGSCCATCTGGAGGAGCAGAAATACTACGGGACTATGGACGCTAC 660  
661 GCGAGGGAGGGAGTCAAGGGCTCTGGAGAAAGGACTTCCACATATGGAAAT 720  
Qy 661 GCGAGGGAGGGAGTCAAGGGCTCTGGAGAAAGGACTTCCACATATGGAAAT 720  
Db 721 GCTATGCTCAATGTGTGAGTGGGACCTCAAGGAGAACTCTCAAGGGAGACTGTGGAC 780  
Qy 721 GCTATGCTCAATGTGTGAGTGGGACCTCAAGGAGAACTCTCAAGGGAGACTGTGGAC 780  
Db 780 TAAAGGGATGGGAGGCTTAGGGAGGCCCTGCGMCCCCCGGGAGGACACGCCA 63  
Qy 781 TACCACTGCTACTGAACTTCCCTGGCTCTCTGCTCTGGGCTCTGGAGGAGCTTC 840  
Db 781 TACCACTGCTACTGAACTTCCCTGGCTCTCTGCTCTGGGCTCTGGAGGAGCTTC 840  
841 TGTGCCCAAGTGTGCTCCGGTGAATGACGGCTATTAATGACTCACT 900  
Qy 841 TGTGCCCAAGTGTGCTCCGGTGAATGACGGCTATTAATGACTCACT 900  
Db 900 CCAAGGCAAGTACTTCAGCCCTCTGGAGTGTGATATAAGATGGCCAGGGCCCC 960  
Qy 901 CCAAGGCAAGTACTTCAGCCCTCTGGAGTGTGATATAAGATGGCCAGGGCCCC 960  
Db 901 CCAAGGCAAGTACTTCAGCCCTCTGGAGTGTGATATAAGATGGCCAGGGCCCC 960  
Qy 961 ACAGCCCTCTACAGGATTACACCTCT 991  
Db 961 ACAGCCCTCTACAGGATTACACCTCT 991

RESULT 6  
US-08-937-466-1  
; Sequence 1, Application US/08937466  
; GENERAL INFORMATION:  
; Patent No. 5846779  
; APPLICANT: Zhang, Ning  
; APPLICANT: Amaral, M. Catherine  
; APPLICANT: Chen, Jin-Long  
; TITLE OF INVENTION: UCP3 Gene  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSE: SCIENCE & TECHNOLOGY LAW GROUP  
; STREET: 75 DENISE DRIVE  
; CITY: HILLSBOROUGH  
; STATE: CALIFORNIA  
; COUNTRY: USA

ZIP: 94010  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/937,466  
FILING DATE: 4/3/2004  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: 197-009  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 343-4341  
TELEFAX: (650) 343-4342  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2782 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-937-466-1  
Query Match Similarity 59.5%; Score 732; DB 2; Length 2782;  
Best Local Similarity 81.1%; Pred. No. 9e-179; 0; Mismatches 195; Indels 15; Gap 4;  
Matches 904; Conservative 0;  
Query 4 TGGGATGGGCTTAGGGAGGCCCTGCGMCCCCCGGGAGGACACGCCA 63  
Db 93 TGGAGTGGAGCTTAGGGCTGGCCCTGCACT-ACCCACACTTGGCTAGACGACAGCTTC 151  
Qy 64 CGCTGCACTGAGGCCAGGCTGTGGAGCAGCCCTCTCTGGACCTCTCGGCC 123  
Db 152 TCCCTGAACTGAGGAAATGGCAGGAGCTCTGGGCTGAGCTCATGGCC 211  
Qy 124 TAAAGGGATGGGAGGCTGGCTTCCAGGAGTGGTGGAGTGGAGGCTCTGAGCTGGCT 183  
Db 212 AAAGGAGACCAAGCCATTCC--CCGGAGACCATGGTGGACTCTCAGGCCCTCGGAAGGCT 269  
Qy 184 CCCACCTGGTGTGAGTGTCTGGGGAGGAGCACAGGAGCTGTTGCGTACCTGTT 243  
Db 270 CCCACACGGTGTGAGTGTCTGGGGCGGGACTGGCTGTC 329  
Qy 244 ACCTTCCACTGGACAGGCCAAAGGCTGGCTGAGATCCAGGGAGAACGGGGTC 303  
Db 330 ACTTTCCTGGACACGCCAGGCTCCGTCAGATCCAGGGAGAACGGGGCT 389  
Qy 304 CAGACGCCGCGCTCTGGAGTGGCTGGCTGGAGGACCATGGTGGCTGAGCTGGCT 363  
Db 390 CAGA-----GGCTGAGTACCCGGGCTGGCTGGCTGGAGTACATCTGACTATGGGGC 440  
Qy 364 ACTGAGGGCTGGAGGCCCTACATGGCTGGCTGCCCTGAGGCCAGATGAG 423  
Db 441 ACAGAGGGTCCCGCAGGCCCTACAGGAGCTGGTGTGCTGCTGCTGAGGT 500  
Qy 4224 TGGCCCTCATGGCGCATGGCTCTGGAGTGGTGTGAGGACCCCAAGGC 483  
Db 501 TTGGCTGCACTGGAGTGGCTCTGGAGTGGTGTGAGGACCTGGAGGG 560  
Qy 484 GGGGAGACACTGGCTCTGGAGTGGCTGGAGGCTGGCTGGAGGCTGGCG 543  
Db 561 GGGGAGACACTGGCTGGAGTGGCTGGAGGCTGGAGGCTGGAGGCTGGAGG 620  
Qy 544 GTGAGCTGGCCAGGCCAGGATGGTGGAGGCTGGCTGAGGCTGGAGGCTGGAGG 603  
Db 621 GTGAGCTGGCCAGGCCAGGATGGTGGAGGCTGGCTGAGGCTGGAGGCTGGAGG 680  
Qy 604 GGACCATGGAGGAGAACATGGAGGACTATGGAGGACTATGGAGGACTATGGAGG 663  
Db 681 GG---ACTGGAGGAGAACATGGAGGACTATGGAGGACTATGGAGGACTATGGAGG 737







ATTORNEY/AGENT INFORMATION:  
 NAME: OSMAN, RICHARD A  
 REGISTRATION NUMBER: 36,627  
 REFERENCE/DOCKET NUMBER: T97-009  
 TELECOMMUNICATION INFORMATION:  
 TELEFAX: (650) 343-4342  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1949 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 US-09-37-466-3

Query Match 57.3%; Score 705.4; DB 2; Length 1949;  
 Best Local Similarity 81.6%; Pred. No. 5.e-172;  
 Matches 869; Conservative 0; Mismatches 181; Indels 15; Gaps 4;

```

QY 4 TGGGATGGCCCTAGGGAGCCCTTGCTGCCCTTGGCGAGGACTCACCCCA 63
Db 93 TGGAGTGGAGCCTTAGGTGACCT-ACCCACCTTC 151
Qy 64 CGCGTGCAGCTGAGCCAGGGCTGGAGCAGCTCTCTGAACTCTCGCCC 123
Db 152 TCCCTGCACTGAGCAAAGATGCGAGGAGCTCTCTCGAACCTCATAGGCAGC 211
Qy 124 TAAGGACTGGAGAGCCCTCCAGACTATGGTGGAGCTGAAACCTTCAAGCT 183
Db 212 AAAGGAGACCAGGCCATTC-CGGGACCATGGTGGAGCTCAGCCTCGAAGGCGCT 269
Qy 184 CCCACCATGGCTGTGAAGTTCTGGGGGACGGACAGCCGCTGGTTGCTGACCTCGT 243
Qy 270 CCACACACGGTTGAGTTCTGGGGGCGACCTCGGCTGTTGCGACCTCTC 329
Qy 244 ACTTTCACAGGACACAGCCAGGGCGCCGAGTCAGCCAGGGAGAACCGCGTC 303
Db 330 ATTTTCCCCTGACACGCCAGGGCGCTGCTGAGTCAGGAGAACCCAGGGCT 389
Qy 304 CAGACGCCCGCTCGTCAAGCTACCGCGCTGGCGCTGGGACACATCTGACCATGGCGGG 363
Db 390 CAGA-----GCGTGCAGTACCGGGTGGCTGGTACATCTGACATGGTGCCC 440
Qy 364 ACTGAGGGCTCCGAGCCCTACATGGTTGGAGCCGCTCAGGCCAGATGAGC 423
Db 441 ACAGAGGCTCCCGAGCCCTACAGGGATGGCTGCTGACCTGACCCGAGATGAGT 500
Db 424 TTGGCTTCACTGAGCATGGCTCTAGCTGGCTGAGGGTGACCCCAAGGC 483
Db 501 TTGCTCTCATGAGTGGCTCTAGCTGGCTGAGGGTGACCCCAAGGA 560
Qy 484 GCGGACRACTCCAGCTCACTACGCCGATTTGGCGGGCTGACCCATGGG 543
Db 561 GGGGACACTCAAGCGTGGCTACAGGTTGGCTGAGGAGGACATGGCAAGGCA 620
Qy 544 GTGACCTGTGCCAGCCAGATGGTGGCTGATTCAGCCAGCATACCTC 603
Db 621 GTGACCTGTGCCAGCCAGCCATGGCTGAGGTGGCTGAGGTCGATTCAACCTC 680
Qy 604 GGGCCATCAGGAGCAAGAAATAAGGGAGCTATGGCAAGGACCATGGC 663
Db 681 GG--AATGGGAGGAGAAATACAGGGAGCATGGATGGCTACAGGACATGGC 737
Qy 664 AGGGAGGAGGGTCAAGGGCTGTGGAAGGACTTGCCACATCAGGGATGT 723
Db 738 AGGGAGGAGGGTCAAGGGCTGTGGAAGGACTTGCCACATCAGGAAATGCC 797
Qy 724 ATGCTCACTGTGCTGAGCTGGACTACGATCTCAAGGAGAGCTGGACTAC 783
Db 798 ATGTCAGCTGTGCTGAGATGGCTACGACATCATCAAGGAGATGGAGCT 857
Qy 784 CACCTGCTGACTGACACTCCCTGCACCTTGCTCTGGCTTGGAGGGCTCTGT 843

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RESULT 11  
 US-09-172-528-3  
 ; Sequence 3, Application US/0912528  
 ; Patent No. 5952469  
 GENERAL INFORMATION:  
 APPLICANT: Zhang, Ning  
 APPLICANT: Amaral, M. Catherine  
 APPLICANT: Chen, Jin-Long  
 TITLE OF INVENTION: UCP3 Genes  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:  
 ADDRESSE: SCIENCE & TECHNOLOGY LAW GROUP  
 STREET: 75 DENISE DRIVE  
 CITY: HILLSBOROUGH  
 STATE: CALIFORNIA  
 COUNTRY: USA  
 ZIP: 94010  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/172,528  
 FILING DATE:  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/937,466  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: OSMAN, RICHARD A  
 REGISTRATION NUMBER: 36,627  
 REFERENCE/DOCKET NUMBER: T97-009  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650) 343-4341  
 TELEFAX: (650) 343-4342  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1949 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 US-09-172-528-3

Query Match 57.3%; Score 705.4; DB 2; Length 1949;  
 Best Local Similarity 81.6%; Pred. No. 5.e-172; Indels 15; Gaps 4;  
 Matches 869; Conservative 0; Mismatches 181;

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Qy 4 TGGGATGGCCCTAGGGAGCCCTTGCTGCCCTTGGCGAGGAGCTACCCCA 63
Db 93 TGGAGTGGAGCCTAGGTGACCT-ACCCACCTTC 151

```

QY 64 CCGCTGCACTGAGGCCAGGGCTGAGGAGGACGCCCTCTCCCTGGCCC 123  
Db 152 TCCCTGACTGAGCAAGAATGCGAGGAAAGCTCTCGGACCTCCATGGCAGC 211  
Qy 124 TAAGGGACTGGCGAGGCTTCCAGGAGTATGGTTGAGCTGAAGCTGGCT 183  
Db 212 AAAGGACCGAGGCCATTCC-CCGGACCATGGTGTGAGCT 269  
Qy 184 CCCACCATGGCTGAGTCTCTGGGGAGGCAGCACCTGTTGACCTCGTT 243  
Db 270 CCCACAACTGTTGAGTCTCTGGGGAGGCAGCACCTGCTGTTGACCTCGTC 329  
Qy 244 ACCTTTCACATGGACAGCGCAAGGTCGCTGAGATCCAGGGAGAACGGGTC 303  
Db 330 ACTTTTCCCTGAGCACCGCAAGGTCGCTGAGATCCAGGGAGAACGGGCT 389  
Qy 304 CAGAGGGCCGCTGCTGCGCTGAGCTGCTGGGGAGGCACCATGCTGGCG 363  
Db 390 CAGA-----GCTGAGTACCGGGTGTGAGGTACCATCTGAGCT 440  
Qy 364 ACTGAGGGTCTGAGCCCCCTACATGGCTGGGGCCGAGGAGCACCTGAGC 423  
Db 441 ACAGGGTCCGGAGCCCTACAGGGACTTGGCTGCTGCTGACGGCAGATGAG 500  
Qy 424 TTCGCTTCCATTCGGCATCGGCCCTATGACTTCGGTCAAGGGTGACCCCCAAGG 483  
Db 501 TTGCTTCCATTCGAAATGGCTCTAGACTCTGTCAAGGGTCTACACCCCAAGGA 560  
Qy 484 GGGGAAACTCTCAGCTCACTACCGGATTGGGGGCTGACCCAGATGGCG 543  
Db 561 GGGGACACTCTAGCTGGCTGCTGAGATCTGGAGGCTGACGAGGCAATGGCA 620  
Qy 544 GTGACCTGTGCCAGCCACGATGGGGTGGAGGGCGATTTCAGCCACATACCTC 603  
Db 621 GTGACCTGTGCCAGCCACGATGGGGTGGAGGGCGATTTCAGCCATACCTC 680  
Qy 604 GGGCCATTCAGGAGCACAGAAATCAGGGACTATGGCTACAGACCATCGCC 663  
Db 681 GG--AACTGGAGGAGGAGGAAATCAGGGACTATGGCTACAGACCATCGCC 737  
Qy 664 AGGGAGGAGGAGGAGTCAAGGGCTGTGAAAGGAACTTGCACACATCAGGAGATG 723  
Db 738 AGGGAGGAGGAGGAGTCAAGGGCTGTGAAAGGAACTTGCACACATCAGGAGATGCC 797  
Qy 724 ATCGTCACTGCTGAGGGTGTGACTACATCTAGGGAGGCGCTGCTGACTAC 783  
Db 798 ATTGTAACCTGTCTGAGATGTGACTACACATCATCAGGAGAGTCTGCTGCT 857  
Qy 784 CACCTCTCACTGAGCAACTCCCTGACTTCTGCTGAGCTCTGCTGCTGCTG 843  
Db 858 AACCTGTTAGTGTGACACTCTCCCTGACTTGTGCTGCTGCTGCTGCTG 917  
Qy 844 GGCACAGTGGCTGCCCTCCGGTGGAGCACCCGTTATGAACTCACTCCA 903  
Db 918 GGCACAGTGGCTGCCCTCCGGTGGAGCACCCGTTATGAACTCACTCCA 977  
Qy 904 GGCAGTACTGAGCCCTGACTGTATGATAAGATGGTGGCCAGGGGCCACA 963  
Db 978 GGCAGGACTACCAGCCGCTCTCAGTGTGAGATGTGGCTGAGGAGGCCAG 1037  
Qy 964 GCCTTCTACAAAGGATTACCCCTTTGCGTTGAGCTCTGGAGCTGGGTGATG 1023  
Db 1038 GCCTTCTACAAAGGATTGCGCTCTTGTGGCTGAGGAGCTGGAGCTGGATG 1097  
Qy 1024 TTGTTACCTTGAGGAGCTAAACGGCCCTGATGAAAGTCAG 1068  
Db 1098 TTGTTACATATGAGCAACTGAGGAGGCCCTAATGAAAGTCAG 1142

GENERAL INFORMATION:  
APPLICANT: Zhang, Ning  
APPLICANT: Amalai, M. Catherine  
APPLICANT: Chen, Jin-Dong  
TITLE OF INVENTION: UCP3 Genes  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 75 DENISE DRIVE  
CITY: HILLSBOROUGH  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94010  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.3.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/318,199  
FILING DATE:  
CLASIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/937,466  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A.  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-009  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 343-3441  
TELEFAX: (650) 343-3442  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1949 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-09-318-199-3

Query Match 57.3%; Score 705.4; DB 3; Length 1949;

Best Local Similarity 81.6%; Pred. No. 5.5e-172;  
Matches 869; Conservative 0; Mismatches 181; Indels 15; Gaps 4;

Qy 4 TGGATGGAGCCCTGGAGGCCCTGGTGGCCCTGCGCTGGAGGACTCACAGCCCA 63  
Db 93 TGGATGGAGCCCTGGAGGCCCTGGTGGCCCTGCGCTGGAGGACTCACAGCCCA 151  
Qy 64 CCGCTGCACTGAGGCCATTC-CCGGACCATGGTGTGAGCT 211  
Db 152 TCCCTGACTGAGCAAGAATGCGAGGAGCTCTCTGACTCTCTGAGCT 183  
Qy 184 CCCACCATGGCTGAGTCTCTGGGGAGGCAGCACCTGTTGTGAGCT 243  
Db 270 CCCACAACTGTTGAGTCTCTGGGGAGGCAGCACCTGTTGTGAGCT 329  
Qy 304 CAGACGGCCCGCTGAGCTGAGTACCTGCTGAGCTGAGCTGAGCT 363  
Db 390 CAGA-----GCTGAGTACCGGGTGTGAGCT 440  
Qy 364 ACTGAGGGTCTGAGGCCCTACATGAGCTGGGGAGGCCCTGAGCTGAGCT 423  
Db 441 ACAGGGTCCGGAGGCCCTACAGGAGCTGAGCTGGGGAGGCCCTGAGCT 500

RESULT 12  
US-09-318-199-3  
Sequence 3 Application US/09318199  
; Patent No. 6025469





STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94010  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.3.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/172,528  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/937,466  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-009  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 343-4341  
TELEFAX: (650) 343-4342  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1777 base pairs  
STRANDEDNESS: double  
TYPE: nucleic acid  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
09-172-528-5

query March 48.2%; Score 593.8; DB 2; Length 1777;  
best Local Similarity 81.2%; Pred. No. 2,7e-13; Indels 15; Gaps 4;  
matches 743; Conservatism 0; Mismatches 157; Gaps 4;

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 4 TGGGATGGGCCCTAGGGAGCCCTGCTGGCCCTGGCTGGAGGACTCACAGCCCCA 63
 93 TCGAGTCAGCCTTAGGGTGGCTTGCACT-ACCCAACCTTGTAGGACAGCTTC 151
 64 CCCCTGCAGCTGAAGGCCAGGGCTGGAGCAGGCCCTCCTGGCCCTGGCTGT 123
 152 TCCCTGAAGCTGAAAGCAAAAGATTCAGGAGGAAAGCTCTCTGGACCTCATAGGAGC 211
 124 TAAGGGACTGSGCAGAGCTTCAAGGACTATGGTGTGAGCTGAGCTTCAGAGCTGT 183
 212 AAAGGAACCCAGGCCATTC - CGGGACCATGGTTGAACTCAGCCCTTCGAGTGCT 269
 184 CCCACCATGCTGTGAGCTCTGGGGAGGACAGAGGCCCTTGTGACTCTT 243
 270 CCCACACAGGTCTGAACTTCCCTGGGCCCGGGACTGTGGCTCTGGACCTCTC 329
 244 ACCTTCCACTGGAACAGCCAAAGTCTCCCTGCAAGATCAGGGGGAGGACAGGGGTC 303
 330 ACTTTCCCTGGAAACCCCAAGGTCTCTGGAGATCAAGGGAGAACCCAGGGCT 389
 304 CAGACGGCCGAGCTGAGTACGGTGGCTGGCTGGAGGCTGGGGCTGGAGGCTGG 363
 390 CAGA-----GGTGTGAGTACGGCTGGCTGGAGGCTGGAGGCTGGAGGCTGG 440
 364 ACTGAGGGCTCTGAGCCCTAGATGGCTGGCTGGGGCTGGAGGCTGGAGGCTGG 423
 441 ACAGAGGCTCCCGCAGGCCCTACAGGGACTGGTGGCTGGAGGCTGGAGGCTGG 500
 484 GGCGACGAACTCCAGCCCTACTACCGGGATTGGCTGGCTGGAGGCTGGAGGCTGG 543
 424 TGGCCTCCTACCGCATGGCTCTATGACTCTCAAGCAGGGTACACCCCAAGGCC 483
 561 GCGGACCACTCCAGGGCTGGCTGAGGCTGGAGGCTGGAGGCTGGAGGCTGG 620
 501 TTGCTCTCATGGCTGGCTGAGGCTGGAGGCTGGAGGCTGGAGGCTGGAGGCTGG 560
 544 GTGACTCTGGCCAGCCCCAGATGGGGAGGGCTGGAGGCTGGAGGCTGGAGGCTGG 603

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Search completed: May 18, 2004, 13:54:02  
Job time : 129 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

### On nucleic - nucleic search, using sw model

Run on: May 18, 2004, 13:51:52 ; Search time 588 Seconds

(without alignments)  
950.575 Million cell updates/sec

Title: US-09-423-410-3

Perfect score: 1231  
Sequence: 1 tcctggatggaggcccttagg.....ttgttgattcaagaac 1231

Scoring table: IDENTITY\_NUC  
Gapext 1.0

Searched: 2947324 seqs, 2269024515 residues

Total number of hits satisfying chosen parameters: 5894648

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

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19: /cgmn_6/ptodata/2/pupnna/US60_PUBCOMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	1231	100.0	1231	Sequence 1, Appli
2	1146.4	93.1	1193	Sequence 1, Appli
3	1145.4	93.0	1192	Sequence 1, Appli
4	981.4	79.7	1132	Sequence 1, Appli
5	981.4	79.7	1132	Sequence 1, Appli
6	490	39.8	1575	Sequence 1, Appli
7	490	39.8	1575	Sequence 1, Appli
8	476.6	38.7	13	Sequence 1, Appli
9	476.6	38.7	1105	Sequence 1, Appli
10	476.6	38.7	1612	Sequence 1, Appli
11	476.6	38.7	1643	Sequence 1, Appli
12	476.6	38.7	1646	Sequence 1, Appli
13	475.6	38.6	930	Sequence 1, Appli
14	475.6	38.6	930	Sequence 1, Appli

§

RESULT 1  
US-09-808-457-1  
Sequence 1, Application US/09808457 05/6/2003

; Sequence 1, Application US/09808457 05/6/2003

; Patent No. US200205239A1

; GENERAL INFORMATION:

; APPLICANT: Boettcher, Brian

; APPLICANT: Caplan, Shari

; APPLICANT: Kaleto, Michael

; APPLICANT: Connely, Sheila

; APPLICANT: Desai, Urvi

; APPLICANT: Sloberg, Eric

; TITLE OF INVENTION: Methods and Compositions For Treatment

; TITTLE OF INVENTION: Of Diabetes and Related Conditions Via Gene Therapy

; FILE REFERENCE: 4-31353A/USN

; CURRENT APPLICATION NUMBER: US/09/808,457

; CURRENT FILING DATE: 2001-03-14

; PRIORITY APPLICATION NUMBER: 60/XXX,XXX

; PRIORITY FILING DATE: 2000-03-15

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 1

; LENGTH: 1231

; TYPE: DNA

; ORGANISM: Unknown

; FEATURE: Other Information: cDNA from clone UCP31

; US-09-808-457-1

; OTHER INFORMATION: Query Match Similarity 100.0%; Score 1231; DB 9; Length 1231; Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

; Matches 1231; Conservative 0;

; Sequence 1, Appli

; Sequence 2, Appli

; Sequence 3, Appli

; Sequence 4, Appli

; Sequence 5, Appli

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; Sequence 9, Appli

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; Sequence 179, Appli



Query Match 93.0% Score 1145.4; DB 9; length 1192;  
 Best Local Similarity 99.9%; Pred. No. 0; Mismatches 1; Indels 0; Gaps 0;  
 Matches 1146; Conservative 0; Mismatches 1;

QY	DB
601	CTCGGCCATCCAGGAGCACAGAAATACGGGGCATATGGGGCTTACAGAACATC 660
646	CTCGGCCATCCAGGAGCACAGAAATACGGGGCATATGGGGCTTACAGAACATC 705
661	GCAAGGAGGAGGTCAAGGCTTGAGGACTTGCCAACTTCATGGGAACTTGAGGAAAT 720
706	GCAAGGAGGAGGTCAAGGCTTGAGGACTTGCCAACTTCATGGGAACTTGAGGAAAT 765
721	GCTATGTCGAACGTGCTGGCTGGGGCTTGAGGACTTGCCAACTTCATGGGAAAT 780
766	GCTATGTCGAACGTGCTGGGGCTTGAGGACTTGCCAACTTCATGGGAAAT 825
781	TACCACTGTCGAACGTGCTGGGGCTTGAGGACTTGCCAACTTCATGGGAAAT 840
826	TACCACTGTCGAACGTGCTGGGGCTTGAGGACTTGCCAACTTCATGGGAAAT 885
841	TGTGCCACAGTGTGGGGCTTGAGGACTTGCCAACTTCATGGGAAAT 900
886	TGTGCCACAGTGTGGGGCTTGAGGACTTGCCAACTTCATGGGAAAT 945
901	CCAGGCCAGTACTTCAGCCCCCTCGACTGTGTTGATAAGATGTGGGGCTTGAGGAAAT 960
946	CCAGGCCAGTACTTCAGCCCCCTCGACTGTGTTGATAAGATGTGGGGCTTGAGGAAAT 1005
961	ACAGCCTCTAACAGGATTACACCTCTTGGGGCTTGAGGACTTGTTG 1020
1006	ACAGCCTCTAACAGGATTACACCTCTTGGGGCTTGAGGACTTGTTG 1065
1021	ATGTTGTAACCTTACGGGGCTTGAGGACTTGAGGACTTGAGGAAAT 1080
1066	ATGTTGTAACCTTACGGGGCTTGAGGACTTGAGGACTTGAGGAAAT 1125
1081	TCCACCTTGTGACAGAACAGAACAGAACAGAACAGTAGTGGAAAT 1140
1126	TACCGTTTGTGACAGAACAGAACAGAACAGAACAGTAGTGGAAAT 1185
1141	AATGGAG 1148
1186	AATGGAG 1193

RESULT 3  
 US-09-734-134-1  
 Sequence 1, Application US/09734134  
 ; Patient No. US20010010929A1  
 ; GENERAL INFORMATION:  
 APPLICANT: Lee James Beeley  
 APPLICANT: Robert James Godden  
 TITLE OF INVENTION: NOVEL COMPOUNDS  
 FILE REFERENCE: GH-30002-D1  
 CURRENT APPLICATION NUMBER: US/09/734,134  
 CURRENT FILING DATE: 2000-12-11  
 PRIOR APPLICATION NUMBER: GB 9704551.2  
 PRIOR FILING DATE: 1997-03-05  
 PRIOR APPLICATION NUMBER: GB 9705614.7  
 PRIOR FILING DATE: 1997-03-18  
 PRIOR APPLICATION NUMBER: EP 97305305.1  
 PRIOR FILING DATE: 1997-07-16  
 PRIOR APPLICATION NUMBER: GB 9800633  
 PRIOR FILING DATE: 1998-03-02  
 PRIOR APPLICATION NUMBER: 09/142,565  
 PRIOR FILING DATE: 1999-06-30  
 NUMBER OF SEQ ID NOS: 6  
 SOFTWARE: FASTSEQ FOR Windows Version 3.0  
 SEQ ID NO 1 LENGTH: 1192  
 TYPE: DNA  
 ORGANISM: HOMO SAPIENS  
 US-09-734-134-1

RESULT 4  
US-09-808-457-3  
; Sequence 3, Application US/09808457  
; Patent No. US20020065339A1  
; GENERAL INFORMATION:  
; APPLICANT: Boettcher, Brian  
; APPLICANT: Caplan, Shari  
; APPLICANT: Kaleko, Michael  
; APPLICANT: Connolly, Sheila  
; APPLICANT: Deal, Uri  
; APPLICANT: Slosberg, Eric  
TITLE OF INVENTION: Methods and Compositions For Treatment  
; TITLE OF INVENTION: Of Diabetes and Related Conditions Via Gene Therapy  
FILE REFERENCE: 4-31333A/USN  
CURRENT APPLICATION NUMBER: US/09/808,457  
CURRENT FILING DATE: 2001-03-14  
PRIOR APPLICATION NUMBER: 60/XXX,XXX  
PRIOR FILING DATE: 2000-03-15  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO: 3  
LENGTH: 1132  
TYPE: DNA  
; FEATURE:  
; ORGANISM: Unknown  
; OTHER INFORMATION: cDNA from clone UCP3S  
US-09-808-457-3

Query Match 79.7%; Score 981.4; DB 9; Length 1132;  
Best Local Similarity 99.4%; Pred. No. 1.1e-27; Matches 985; Conservativeness 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TCTCTGGGATGGAGGCCCTAGGAGAGCCCTGTGCTGCCCTGTGCGTGGAGAGCTCAAGCC 60  
Db 1 TCTCTGGGATGGAGGCCCTAGGAGAGCCCTGTGCTGCCCTGTGCGTGGAGAGCTCAAGCC 60

QY 61 CCACCCGTCGACTGAGCCCGGGCTGGAGCAGCTCTCTCTGGACCTCTCTGGCG 120  
Db 61 CCACCCGTCGACTGAGCCCGGGCTGGAGCAGCTCTCTGGCG 120

QY 121 CCTTAAGGGCTGGAGAGGCCTTCAGGACTATGGTGAAGCTGAGCTTCAGAGCTG 180  
Db 121 CCTTAAGGGCTGGAGAGGCCTTCAGGACTATGGTGAAGCTGAGCTTCAGAGCTG 180

QY 181 CCTCCCAACCATGGCTGTGAAAGTCCTGGGGGAGGCAAGAGCTGTTTGCTGACCTC 240  
Db 181 CCTCCCAACCATGGCTGTGAAAGTCCTGGGGGAGGCAAGAGCTGTTTGCTGACCTC 240

QY 241 GTTACCTTCCTCTGGACACGCCAACGGTCCTCTGAGTCAGGGAGAACCGGG 300  
Db 241 GTTACCTTCCTCTGGACACGCCAACGGTCCTCTGAGTCAGGGAGAACCGGG 300

QY 301 GCGAGAGGGCCGGCTGGCTGAGTACGTGCTGGCTGCTGGCACCCATCTTACCTGG 360  
Db 301 GCGAGAGGGCCGGCTGGCTGAGTACGTGCTGGCTGCTGGCACCCATCTTACCTGG 360

QY 361 CGGACTGAGGTGCTCTGAGGCCCTACATGGCTGTGGGGCTGCAAGGCCAGATG 420  
Db 361 CGGACTGAGGTGCTCTGAGGCCCTACATGGCTGTGGGGCTGCAAGGCCAGATG 420

QY 421 AGCTTCGCCCCATCCGATCGGCCCTATGACTCCGTCAGGAGGTTGACACCCAAA 480

RESULT 5  
US-09-823-886A-5  
; Sequence 5, Application US/09823886A  
; Publication No. US20030150022A1  
; GENERAL INFORMATION:  
; APPLICANT: Newell, Martha  
; APPLICANT: Berry-Lowe, Sandra  
TITLE OF INVENTION: Compositions and methods for regulating metabolism in Plants  
FILE REFERENCE: C11027/002  
CURRENT APPLICATION NUMBER: US/09/823, 886A  
CURRENT FILING DATE: 2001-03-30  
PRIOR APPLICATION NUMBER: US 60/193, 533  
PRIOR FILING DATE: 2000-01-31  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: Patentin version 3.0  
SEQ ID NO: 5  
LENGTH: 1132  
TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-823-886A-5

Query Match 79.7%; Score 981.4; DB 10; Length 1132;  
Best Local Similarity 99.4%; Pred. No. 1.1e-27; Matches 985; Conservativeness 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TCTCTGGGATGGAGGCCCTAGGAGAGCCCTGTGCTGCCCTGTGCGTGGAGAGCTCAAGCC 60  
Db 1 TCTCTGGGATGGAGGCCCTAGGAGAGCCCTGTGCTGCCCTGTGCGTGGAGAGCTCAAGCC 60

QY 61 CCACCCGTCGACTGAGCCCGGGCTGGAGCAGCTCTCTGGCG 120  
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FILE REFERENCE: 44921-5039-US  
 CURRENT APPLICATION NUMBER: US/09/917, 800A  
 CURRENT FILING DATE: 2001-07-31  
 PRIOR APPLICATION NUMBER: US 60/222, 040  
 PRIOR APPLICATION DATE: 2000-07-31  
 PRIOR APPLICATION NUMBER: US 60/222, 880  
 PRIOR APPLICATION DATE: 2000-11-02  
 PRIOR APPLICATION NUMBER: US 60/290, 029  
 PRIOR FILING DATE: 2001-05-11  
 PRIOR APPLICATION NUMBER: US 60/297, 457  
 PRIOR FILING DATE: 2001-05-15  
 PRIOR APPLICATION NUMBER: US 60/292, 336  
 PRIOR FILING DATE: 2001-05-22  
 PRIOR APPLICATION NUMBER: US 60/295, 798  
 PRIOR FILING DATE: 2001-06-06  
 PRIOR APPLICATION NUMBER: US 60/299, 645  
 PRIOR FILING DATE: 2001-06-13  
 PRIOR APPLICATION NUMBER: US 60/298, 884  
 PRIOR FILING DATE: 2001-06-19  
 PRIOR APPLICATION NUMBER: US 60/303, 459  
 PRIOR FILING DATE: 2001-07-09  
 NUMBER OF SEQ ID NOS: 1740  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 1679  
 LENGTH: 1575  
 TYPE: DNA  
 ORGANISM: Rattus norvegicus  
 FEATURE:  
 OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM\_019354  
 US-09-917-800A-1679  
 Query Match 39.8%; Score 490; DB 9; length 1575;  
 Best Local Similarity 71.3%; Pred. No. 2.6e-133; 0; Mismatches 265; Indels 15; Gaps 3;  
 Matches 694; Conservative 0;  
 Query 147 CCGGACTATGGTGGCTGAGCCTGCCTCCACCATGGCTGTGAGCTGCTCC 206  
 Db 338 CAGAACTCTGGTGGTTCAAGGCCACGGAGTGCCCCCACGCCACCGAGTCT 397  
 Query 207 GAGGGAGGAGAGAGGAGGAGGAGGAGGAGGACTTCACCCAGGAGAAC 266  
 Db 398 GGG 457  
 Query 721 GGTATCGTCAACTGGTGGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 780  
 Db 781 TACCACTGCTRACTGACAACCTCCCCTGCCACTTGTCTCCCTTGGGCCGGTC 840  
 Query 781 TACCACTGCTRACTGACAACCTCCCCTGCCACTTGTCTCCCTTGGGCCGGTC 840  
 Db 841 TGGGCCAGTGGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 900  
 Query 841 TGGGCCAGTGGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 900  
 Db 901 CGAGGCCAGTACCTTACGCCCTTGACTGTATGATAAGATGATGACTCT 960  
 Query 901 CGAGGCCAGTACCTTACGCCCTTGACTGTATGATAAGATGATGACTCT 960  
 Db 961 AGAGCCTCTACAGGGATTAGACCCCTCT 991  
 Query 961 AGAGCCTCTACAGGGATTAGACCCCTCT 991  
 Db 961 AGAGCCTCTACAGGGATTAGACCCCTCT 991  
 RESULT 6  
 US-09-917-800A-1679  
 ; Sequence 1679, Application US/09/917,800A  
 ; Patent No. US20020119462A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mandrick, Donna  
 ; APPLICANT: Porter, Mack  
 ; APPLICANT: Johnson, Kory  
 ; APPLICANT: Castle, Arthur  
 ; APPLICANT: Elashoff, Michael  
 ; APPLICANT: Gene Logic, Inc.  
 ; TITLE OF INVENTION: Molecular Toxicology Modeling



Db 1286 TGTGACCTGGGCC 1299

Remaining Prior Application data removed - See File wrapper or PALM.  
NUMBER OF SEQ ID NOS: 230  
SOFTWARE: CuraSeqList version 0.1  
SEQ ID NO: 131  
LENGTH: 960

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE: CDS

NAME/KEY: CDS

LOCATION: (15)..(941)

US-10-336-472-131

Query Match 38.7%; Score 476.6; DB 13; Length 960;  
Best Local Similarity 71.2%; Pred. No. 1.9e-129; Indels 15; Gaps 3;  
Matches 677; Conservative 0; Mismatches 259;

Db 147 CAGGACTATGGTGGACTGAAGCCTTGAGCTGCCTCCACCGCTTGAACTCT 206  
Qy 8 CAGCACTATGGTGGCTTCAGGCCAGAGTGGCCCTACTGGCACTTGAACTCT 67

Db 68 TGGGTGGCAAGCTGGCATGGCATCCATCACCTTCCTGGATACTGCTAA 127

Db 267 GTCCTCGCTGAGATCCAGGGAGAACAG---CGGTCAAGACGCCCGCTCNGA 323

Db 128 AGTCCTGTTACAGATCAAGGAAAGTCAAGGCCAGTCAGGCCAGTCAGGCCA 187

Db 324 CTACAGTGGCTGCTGGACCATCTGACCATTGGGGACTGAGGGCCCTGCAACC 383

Db 188 GTCACCGCTGTGATGGACCATCTGACCATTGGGGACTGAGGGCCCTGCAACC 247

Db 384 CTACAGTGGCTGCTGGACCATCTGACCATTGGGGACTGAGGGCCCTGCAACC 443

Db 248 CTACAGTGGCTGCTGGACCATCTGACCATTGGGGACTGAGGGCCCTGCAACC 307

Db 444 CTCTATGACTCGTCAGCAGGGTGTACCCCCAAGGCCGAGAACCTCGCTAC 503

Db 308 CTGTGATGTCCTGTCAGCTGTCAC---CCAGGCTCTGAGCATGCCAGATGG 364

Db 504 TACCGGATTTGGCCCGCTGACCAACAGGACCATCGGGTGGACTGTGCCAGCCC 563

Db 365 GAGCCSCTCTAGCAGGACCAAGGCCGCTTCAGGCCAC 424

Db 564 AGATGTTGGAGGTCGATTTCAGCCAGATAACCTCGGCCATCCAGGACAG 623

Db 425 GATGTTGGTAAGTCGATTCAAGC-----TAGCCCGGGTGGAGGTGTC 475

Db 624 AAAATCAGCGGGACTATGGAGGCTTACAGACCATTCGGCCAGGGAGGG 683

Db 476 GAGATCCAAGCACCCTAATGCCATACAGGATGCTATGCAATCTGGT 535

Db 684 CTGTGAAAGAAGACTTGCCCAACATCATCAGGAATGCTATGCAATCTGGT 743

Db 536 CCTCTGAAAGGACCTCTCCATGTTGCTCACTGCTGAACTGCTGAGCT 595

Db 744 GGTGACCTACGACATCTCAAGGAGAGCTGCTGGACTTCACTGACACT 803

Db 596 GTGACCTATGACTCTCATCAAGATECCCTCTGAAAGCCACTCTGAGATGACT 655

Db 804 CCCCTGCACTTGTCTGGCTTGGCGCGCTCTGTCACAGTGGTGGCTCCTCCC 863

Db 656 CCTTGCCACTCTCACTCTGCTTGGCAGGCTCTGACCACTCTGACGCTCCC 715

Db 864 GGTGAGCTGGAGAACCCGTTAACTCACCTTCAGGCAACTCTGAGCCCT 923

Db 716 TGTAGACTGGTCAGAGGAGATACAGTCACTGCTGGCCAGGAGTCACTGCTGG 775

Db 924 CGACTGTGATGAAAGTGGTGGCCAGGGCCACAGCTCTCACAGGGATTC 983

Db 776 CCACTGCGCTTACCTCTCCAGAAGGAGGGCCCCGACCTCTACAGGGTTCA 835

Db 984 ACCCTCTTTCGCTTGGATCTCTGGAAAGCTGGTGTGCTAACCTGAGGAGCT 1043

RESULT 8

Sequence 131, Application US/10336472

PUBLICATION No. US20040043929A1

GENERAL INFORMATION:

APPLICANT: Anderson, David W.

APPLICANT: Ballinger, Robert A.

APPLICANT: Baumgartner, Jason C.

APPLICANT: Burgess, Catherine E.

APPLICANT: Casman, Stacie J.

APPLICANT: Chant, John S.

APPLICANT: Berghs, Constance

APPLICANT: Gangolli, Bisha A.

APPLICANT: Edinger, Shlomit R.

APPLICANT: Elleman, Karen

APPLICANT: Furtak, Katarzyna

APPLICANT: Gerlich, Valerie

APPLICANT: Gilbert, Jennifer A.

APPLICANT: Gunther, Erik

APPLICANT: Gorman, Linda

APPLICANT: Guo, Xiaojia Sasha

APPLICANT: Ji, Weizhen

APPLICANT: Li, Li

APPLICANT: Liu, Xiaohong

APPLICANT: Miller, Charles E.

APPLICANT: Millet, Isabelle

APPLICANT: Padigaru, Muralidhara

APPLICANT: Patturajan, Meera

APPLICANT: Rastelli, Luca

APPLICANT: MacDougal, John R.

APPLICANT: Mishra, Vishnu

APPLICANT: Pena, Carol E.A.

APPLICANT: Spaderna, Steven K.

APPLICANT: Shimkets, Richard A.

APPLICANT: Smithson, Glenna

APPLICANT: Spytek, Kimberly A.

APPLICANT: Stone, David J.

APPLICANT: Shenvoy, Suresh G.

APPLICANT: Ort, Tatiana

APPLICANT: Taurier Jr, Raymond J.

APPLICANT: Tchernov, Velizar T.

APPLICANT: Vernet, Corinne A.M.

APPLICANT: Wolenc, Adam R.

APPLICANT: Zerhusen, Bryan D.

TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

FILE REFERENCE: 21402533C

CURRENT FILING DATE: 2003-01-03

PRIOR APPLICATION NUMBER: 09/746,491

PRIOR FILING DATE: 2000-12-20

PRIOR APPLICATION NUMBER: 10/005,041

PRIOR FILING DATE: 2001-12-04

PRIOR APPLICATION NUMBER: 10/023,681

PRIOR FILING DATE: 2001-12-18

PRIOR APPLICATION NUMBER: 10/024,212

PRIOR FILING DATE: 2001-12-18

PRIOR APPLICATION NUMBER: 10/055,569

PRIOR FILING DATE: 2001-10-26

PRIOR APPLICATION NUMBER: 10/080,334

PRIOR FILING DATE: 2002-02-21

PRIOR APPLICATION NUMBER: 10/092,900

PRIOR FILING DATE: 2002-03-07

PRIOR APPLICATION NUMBER: 10/136,826

PRIOR FILING DATE: 2002-05-01

PRIOR APPLICATION NUMBER: 10/236,417

PRIOR FILING DATE: 2002-09-06

PRIOR APPLICATION NUMBER: 60/345,092

PRIOR FILING DATE: 2002-01-04

RESULT 9  
US-09-823-886A-3  
; Sequence 3, Application US/09823886A  
; GENERAL INFORMATION:  
; Publication No. US20030150022A1  
; APPLICANT: Newell, Martha  
; TITLE OF INVENTION: Compositions and methods for regulating metabolism in plants  
; FILE REFERENCE: C1102/7002  
; CURRENT APPLICATION NUMBER: US/09-823-886A  
; CURRENT FILING DATE: 2001-03-30  
; PRIORITY APPLICATION NUMBER: US 60/193,533  
; PRIORITY FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO: 3  
; LENGTH: 1105  
; TYPE: DNA  
; ORGANISM: Homo sapiens

Query Match 38.7%; Score 476.6; DB 10; Length 1105;  
Best Local Similarity 71.2%; Pred. No. 2e-129; Mismatches 0; Matches 677; Conservative 0; Indels 15; Gaps 3;

Qy 147 CAGGACTATGGTGGACTGAGCTTCAGACGCGCCATGCTTGAAAGTTCT  
Db 82 CACCATGTGTTGGTTCAAGCCACGATGCGCCATGCTTGAAAGTTCT 141  
Qy 207 GGGGAGGACACAGCAGCGCTTGTGACTGCTGTGAACTTCCACTGGAACAGCAA 266  
Db 142 TGGGCTGAGCTGCTGCTGCTGATGCTGAGCTTCATCACCTTCCTGATACTGTTAA 201  
Qy 267 GTCGCGCTGAGATCAGGGGAGAACAGG--CGTCTCAGACGCCCTCGTGTCA 323  
Db 202 AGTCGGTTACAGATCAGGAGAAGTCAGGGCTGAGCTGAGCGCCCA 261  
Qy 324 GTCGCGCTGCTGCGACCATCTCTGACATGAGCTGGAGTCCTGCAGCCC 383  
Db 262 GTCGCGCTGCTGAGCTGAGCTGAGGGGAACTCCGAGGCT 321  
Qy 384 CTACATCGCTGTGGCGCTGAGCGGAGCTGCTCCATCGATGG 443  
Db 322 CTACATCGCTGTGGCGCTGAGCGGAGCTGCTCCATCGATGG 381  
Qy 444 CCTCTATCTCGTCAAGCGCTGACACCCCAAGGGCGACACTCCMGCCTAC 503  
Db 382 CCTGTATGATTCTGTCACAGTCTACA--CAGGCTCTGAGCTGCAGATGG 438  
Qy 504 TACCGGATTGCGCTGCGCTGACACGGACATACACTCGGCGACCTGCGCAGGCCAC 563  
Db 439 GAGCGCTCTCTGACGAGCACACAGGCTGCGCTGCGCAGGCCAC 498  
Qy 564 AGATGGTGAAGGAACTTCTCCACATCTGAGCATGCTGAGCTGCTGCGCT 623  
Db 499 GGATGTGGTAAGTCGATTCAGC-----TAGGCGGAGCTGAGGTGTTG 549  
Qy 624 AAATACAGGGGACTATGAGCAGGACATCGCCAGGAGGAGGAGCTCA 683  
Db 550 GAGATACCAAGCAGCTGATGCTACAGGACATGCGGAGGAGGAGGCTCGGG 609  
Qy 684 CCTCTGGAAGGAAGTCTGCGCTACATCTGAGCATGCTGAGCTGCTGAGCT 743  
Db 610 CCTCTGGAAGGAAGCTCCAGCTGAGCTGAGCTGAGCTGAGCT 669

RESULT 10  
US-10-265-689-13  
; Sequence 13, Application US/10265689  
; Publication No. US2003011975A1  
; GENERAL INFORMATION:  
; APPLICANT: SURWIT, RICHARD S.  
; APPLICANT: COLLINS, SHEILA A.  
; APPLICANT: WARDEN, CRAIG H.  
; APPLICANT: SELDIN, MICHAEL F.  
; APPLICANT: RICQUER, DANIEL  
; APPLICANT: BOUILAUD, FREDERIC  
; TITLE OF INVENTION: RESPIRATION UNCOUPLING PROTEIN  
; FILE REFERENCE: 1579-376  
; CURRENT APPLICATION NUMBER: US/10/265, 689  
; CURRENT FILING DATE: 2002-10-08  
; PRIORITY APPLICATION NUMBER: US/09/353, 645  
; PRIORITY FILING DATE: 1999-07-15  
; PRIORITY APPLICATION NUMBER: PCT/US97/06864  
; PRIORITY FILING DATE: 1997-04-22  
; PRIORITY APPLICATION NUMBER: 60/034, 960  
; PRIORITY FILING DATE: 1997-01-15  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO: 13  
; LENGTH: 1612  
; TYPE: DNA  
; ORGANISM: Homo sapiens

Query Match 38.7%; Score 476.6; DB 15; Length 1612;  
Best Local Similarity 71.2%; Pred. No. 2.3e-129; Mismatches 0; Matches 677; Conservative 0; Indels 15; Gaps 3;

Qy 147 CAGGACTATGGTGGACTGAGCTTCAGACGCGCTTGTGAACTTCT 206  
Db 338 CACCATGTGTTGGTTCAAGCCACGATGCTGCGCTGCGCTGAGTTCT 397  
Qy 207 GGGGAGGACACAGCAGCGCTTGTGACTGCTGTGAACTTCTGGAACAGCAA 266  
Db 398 TGGGCTGAGCTGCTGCTGCTGAGCTGAGCTGAGCTGAGCTGAGCT 457  
Qy 267 GTCGCGCTGAGCTGAGGGAGAACAGG--CGTCTCAGACGCCCTCGTCA 323  
Db 458 AGTCGGTTACAGATCAGGAGAAGTCAGGGCTGAGCTGAGCTGAGCT 517  
Qy 324 GTCGCGCTGCTGCGACCATCTCTGACATGAGCTGGAGCTGAGCTGAGCC 383  
Db 518 GTCGCGCTGCTGCGACCATCTCTGACATGAGCTGGAGCTGAGCTGAGCC 577

QY 384 CTACATGGGCTGGAGCCGCCTCGAGCSCAGTGAGCTTGACTCCATCG 443  
Db 578 CTACATGGGCTGGTGTGCGCCGCTCGAGCSCAAATGAGCTTGCGCATCG 637  
QY 444 CCTCTATGACTCCGTCAGAGGGTACACCCAAAGGGGAGACTCGCCATCG 503  
Db 638 CCTGATGATCTGTCAGAACGGTCTACA - - CCAAGGCTTGAGCATCGATGG 694  
QY 504 TACCEGGATTGGCGGCGACCCACAGGAGCCATGGCTGACCTGCCAAC 563  
Db 695 GAGCCGCTCTAGCAGGAGCACACAGGCTGGCTGGCTGGACCCAC 754  
QY 624 AAATAAGCGGAGCTATGGAGGCTACAGAACCATGCCAGGGAGAGTCGGG 683  
Db 564 AGATGGTGGAGGTCGATTAGCCAGATACACCTCGGCCATCCAGGAGACAG 623  
Db 755 GGATGTTGTAAGGTCGATTCAGC- - - - - TCAAGGCCGGCTGGTGTGCG 805  
QY 806 GAGATCCAAAGCACCGTCATGGCTACAAGACATGGCCAGGAGAASGGTTCGGG 865  
QY 684 CCTGTGAAAGGAACTTGTGCCAACATCATGGGAATGCTATCGTCACTGTGCTGGT 743  
Db 866 CCTCTGGAAAGGACCTCTCCAAATGTTGCTGTAATGCCATGTCAGCTGCTGAGT 925  
QY 744 CCTGACTTACACATCCTCAAGGAGAGCTGGACTACCTCTACTGACATT 803  
Db 926 GTGACTCTATGAACTCATCAAGGATGCCCTCTGAAGGCCAACTCATGAGCT 985  
QY 804 CCCTGCACTTGTCTGCCCTGGAGGCCGCTCTGTGCCACAGTGGTGGCTCCC 863  
Db 1046 TCTAGAGGTTGCAAGGAGGATACATGAACTCTGCCCTGGCCAGTAGCTGG 1105  
QY 924 CGACTGATGATAAGATGGCCAGGAGGCCACAGCTCTAACAGGGATTAC 983  
Db 1106 CCACTGCCCCCTACCATGTCAGAGGAGGCCGAGCTTCAAAAGGTTCTAC 1165  
QY 984 ACCCTCTTTGGTTGGATCTCTGAAACTGGTGTGTGTAACCTATGAGGT 1043  
Db 1166 GCCTCTTTCTCGCGCTGGCTTCCTGAAACTGGTGTGTGTAACCTATGAGGT 1225  
QY 1044 GAACGGGCCCTGATGAAAGTCAGATGTTAGGGAAATCACCGTTGAC 1094  
Db 1226 GAAACGAGGCCCTATGGCTGCACTTCCGGAGGGCTCTCTGAGC 1276

---

RESULT 11  
US-10-240-965-183  
; Sequence 183, Application US/10240965  
; Publication No. US2003016592A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: SHIFFMAN, Dov  
; APPLICANT: SOMOGI, Roland  
; APPLICANT: LAWN, Richard M.  
; APPLICANT: SEITHAMER, Jeffrey J.  
; APPLICANT: PORTER, Gordon J.  
; APPLICANT: MIKITA, Thomas  
; TITLE OF INVENTION: GENES EXPRESSED IN FOAM CELL DIFFERENTIATION  
; FILE REFERENCE: PA-0025 PCT  
; CURRENT APPLICATION NUMBER: US/10240,965  
; CURRENT FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: 60195,106  
; NUMBER OF SEQ ID NOS: 276  
; SOFTWARE: PERL Program  
; LENGTH: 1643

; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US2003016592A1 093687-6.

Query Match 38.7%; Score 476 6; DB 15; Length 1643;  
Best Local Similarity 71.2%; Pred. No. 2.3e-129; Matches 677; Conservative 0; Mismatches 259; Indels 15; Gaps 3;

US-10-240-965-183

Db 147 CAGGACTATGTTGACTGAGGCTTCATGAGTGCCTCCACATGGCTGAAGTTCT 206  
Db 366 CAGCATCATGTTGGCTTACAGGCAAGATGTTGCGCCCTACTGCACTGTTCT 425  
Db 207 GGGGAGGCAAGGAGCCCTGGTGTGACTCTGCTTACTGCTTCACTGGCACACCAA 266  
Db 426 TGGGTGGCACAGTGTCTCATGCAAGTCTCATCACCTTCCTGATACTGCTAA 485  
Qy 267 GGTCCACCTGAGATCGAGGGAGACCTGG--CGGTCAAGAGGCGCCGCTGTCA 323  
Db 486 ATGCCGTTACAGTCATGAGCTTCAAGGAGAAGCTGAGGCGCTACAGCAGGCCA 545  
Qy 324 GTACCTGGCTGCTGGCACCATCTGACATGTCATGTCAGCTGCTGAGCC 383  
Db 546 GTACCGGGTGTGATGGCACCATCTGACCATGTTGCTGACTGAGGCCCCGAGCT 605  
Qy 384 CTACATGGTGGTACAGGAGCTGGCTGAGCGCGAGTGAATCGCTTCATCCGATCG 443  
Db 606 CTACATGGTGGTGCCTGCGCTGAGCCTGAGCCTAACATGACCTGCTGCG 665  
Qy 444 CCTCTATGACTCCGTCAGAGGAGACACCCAAAGGCCAGACACCTGACCTAC 503  
Db 666 CCTGTTATGATTCTGTCACAGGTTCTAC - - CCAAGGCTCTGACATGCCAGCTGG 722  
Qy 504 TACCGATTTGGCGCTGACCTGAGGAGCTGGCTGAGGAGCTGGCTGAGCC 563  
Db 723 GAGCCGCTCTGAGGAGGAGCTGGCTGAGGAGCTGGCTGAGGAGCTGGCTGAGCC 782  
Qy 564 AGATGGTGGAGGTCGATTTCAGGAGCATACCTCGGCCATCAGGAGGACAG 623  
Db 783 GGATGTTGTAAGGTTGCAAGC- - - - - TCAAGCCCTGGCTGGAGGTGTG 833  
Qy 624 AAATAAGCGGAGCTATGGAGGCCACCTAACGAGGACATGGCCAGGGAGAGTCGGG 683  
Db 834 GAGATACCAAGAACCCCTAACGAGGACATGGCCAGGGAGAGTCGGG 893  
Qy 684 CCTGATGAAAGGAACTTGGCCACATCTGAGGATGTTATGTCACATGCTGAGT 743  
Db 894 CCTCTGGAAAGGACCTCTCCATGTTGCTGTTGAGGAGCTGGCTGAGCT 953  
Qy 744 GTGACCTACGACATCTCAGGAGAGCTCTGAGTACACTCTCTACTGACATT 803  
Db 954 GTGACCTATGACTCTCATGGATGCCCTCTGAGAAGCAACTCATGAGATGACT 1013  
Qy 804 CCCCTGACCTTGTCTGCTGCTTGGCGGCTCTGAGCAGTGGTGGCTCT 863  
Db 1014 CCTTGACCTCTACTCTGCTTGGCGGCTCTGAGCAGTGGTGGCTCT 1073  
Qy 864 GTGGAGCTGGTGAAGGCCGCTATGAACTCTGAGGCTCTGAGCAGTGGTGGCTCT 923  
Db 1074 TGTAGACTGGTCAAGAGGAGATACATGACTCTGCCCTGGCGGAGCTAGTAGCTGG 1133  
Qy 924 CGACTGATGATAAGGTTGGCTGGCGAGGAGGCCACAGSCTCTCATAGGGATTAC 983  
Db 11134 CCTCTGCCCCCTACCATGTCAGAGGAGGCCGCGCCGAGCTTCTACAAAGGTTCTAC 1193  
Qy 984 ACCCTCTTTGGTTGGAGATCTGAGGAGGCTGGTGTGACTATGAGGT 1043  
Db 1194 GCCTCTTTCTCGCGCTGGCTTGGCTGGAGGAGGGTGTGACTATGAGGT 1253  
Qy 1044 GAACGGGCCCTGATGAAAGTCAGATGTTAGGGAAATCACCGTTGAC 1094

Db 1254 GAAACGAGCCCTCATGGCTGCACTCCGGAGGGCTCCTTGAGC 1304  
; ORGANISM: Homo sapiens  
; TYPE: DNA  
; SEQ ID NO: 344  
; LENGTH: 1646  
; US-10-159-563-344

Query Match 38.7%; Score 476.6; DB 16; Length 1646;  
Best Local Similarity 71.2%; Pred. No. 2.3e-129; Matches 677; Conservative 0; Mismatches 259; Indels 15; Gaps 3; Applicant: Meltsar, Paul  
Title of Invention: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR  
FILE REFERENCE: 11613\_56US11  
CURRENT FILING DATE: 2002-12-09  
PRIORITY APPLICATION NUMBER: US 10/133,937  
PRIOR FILING DATE: 2002-04-25  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: Patentin version 3.1

Db 962 GGTGAACCTATGACCACTCATCAGGATGCCCTCGAAGGCCACCTCATGACAT 1021  
; Sequence 7, Application US/09884814  
; Patent No. US20020127600A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Jin-Iong  
; APPLICANT: Amaral, M. Catherine  
; APPLICANT: Tularik Inc.  
; TITLE OF INVENTION: Human Uncoupling Protein 2 (hUCP2): Compositions and  
; Methods of Use  
; FILE REFERENCE: 018781-001110US  
; CURRENT FILING DATE: 2001-05-18  
; PRIORITY APPLICATION NUMBER: US 09/884, 814  
; CURRENT FILING DATE: 2001-05-18  
; PRIORITY APPLICATION NUMBER: US 09/124, 293  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO: 7  
; LENGTH: 930  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURES:  
; NAME/KEY: CDS  
; LOCATION: (1)..(930)  
; OTHER INFORMATION: human uncoupling protein 2 (hUCP2), Fleury et al.  
; US-09-884-814-7

Query Match 38.6%; Score 475.6; DB 9; Length 930;  
Best Local Similarity 71.4%; Pred. No. 3.8e-129; Matches 673; Conservative 0; Mismatches 254; Indels 15; Gaps 3; Applicant: Khan, Javed  
Title of Invention: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS  
FILE REFERENCE: 11613\_56US11  
CURRENT FILING DATE: 2002-12-09  
PRIORITY APPLICATION NUMBER: US 10/159,563  
PRIOR FILING DATE: 2002-04-25  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: Patentin version 3.1

Db 804 CCCCTGCACATTTGCTCTACCTTGGAGCGGCTTCCTGCTCCACAGTGGCTCCC 863  
; Sequence 344, Application US/10159563  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Javed  
; APPLICANT: Ringner, Markus  
; APPLICANT: Peterson, Carsten  
; APPLICANT: Meltsar, Paul  
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR  
; CURRENT FILING DATE: 2002-12-09  
; PRIORITY APPLICATION NUMBER: US 10/133,937  
; PRIOR FILING DATE: 2002-04-25  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO: 344  
; LENGTH: 1646  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-10-159-563-344

Db 864 GGTGGACGTGGTGAAGACCCGGTATATGAACTCACCTCCAGGCGAGCTCAGGCCCT 923  
; Sequence 344, Application US/10159563  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Javed  
; APPLICANT: Ringner, Markus  
; APPLICANT: Peterson, Carsten  
; APPLICANT: Meltsar, Paul  
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR  
; CURRENT FILING DATE: 2002-12-09  
; PRIORITY APPLICATION NUMBER: US 10/133,937  
; PRIOR FILING DATE: 2002-04-25  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO: 344  
; LENGTH: 1646  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-10-159-563-344

Db 1082 TGTAGAGTGGTCAGAGAGATACTGAACTCTGGCGAGGCTCTGACACTGTATGCCCT 1081  
; Sequence 344, Application US/10159563  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Javed  
; APPLICANT: Ringner, Markus  
; APPLICANT: Peterson, Carsten  
; APPLICANT: Meltsar, Paul  
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR  
; CURRENT FILING DATE: 2002-12-09  
; PRIORITY APPLICATION NUMBER: US 10/133,937  
; PRIOR FILING DATE: 2002-04-25  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO: 344  
; LENGTH: 1646  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-10-159-563-344

Db 924 CGACTGTATGATAAAGATGTTGGCCAGAGGGGGCCACGCGCTTACAGGATTAC 983  
; Sequence 344, Application US/10159563  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Javed  
; APPLICANT: Ringner, Markus  
; APPLICANT: Peterson, Carsten  
; APPLICANT: Meltsar, Paul  
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR  
; CURRENT FILING DATE: 2002-12-09  
; PRIORITY APPLICATION NUMBER: US 10/133,937  
; PRIOR FILING DATE: 2002-04-25  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO: 344  
; LENGTH: 1646  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-10-159-563-344

Db 1142 CCACTTGGCCCTTACCATGCTCCAGAAGGAGGGCCCGACCTCTACAGGGATTAC 1201  
; Sequence 344, Application US/10159563  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Javed  
; APPLICANT: Ringner, Markus  
; APPLICANT: Peterson, Carsten  
; APPLICANT: Meltsar, Paul  
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR  
; CURRENT FILING DATE: 2002-12-09  
; PRIORITY APPLICATION NUMBER: US 10/133,937  
; PRIOR FILING DATE: 2002-04-25  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO: 344  
; LENGTH: 1646  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-10-159-563-344

Db 984 ACCTCTTTTGCGTTGGACCTCTGGAACTGTGTGATGTTGACCTATGAGCAGT 1043  
; Sequence 344, Application US/10159563  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Javed  
; APPLICANT: Ringner, Markus  
; APPLICANT: Peterson, Carsten  
; APPLICANT: Meltsar, Paul  
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR  
; CURRENT FILING DATE: 2002-12-09  
; PRIORITY APPLICATION NUMBER: US 10/133,937  
; PRIOR FILING DATE: 2002-04-25  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO: 344  
; LENGTH: 1646  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-10-159-563-344

Db 1202 GCCTCTTCTCCCTTGCTTGGCTTGTGACCTGGTGTGAGCTTGTCACCTATGAGCAGT 1261  
; Sequence 344, Application US/10159563  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Javed  
; APPLICANT: Ringner, Markus  
; APPLICANT: Peterson, Carsten  
; APPLICANT: Meltsar, Paul  
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR  
; CURRENT FILING DATE: 2002-12-09  
; PRIORITY APPLICATION NUMBER: US 10/133,937  
; PRIOR FILING DATE: 2002-04-25  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO: 344  
; LENGTH: 1646  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-10-159-563-344

Db 1262 GAAACGGCCCTGATGAAAGTCAGATGTTACGGGAATACCGTTTGAAC 1094  
; Sequence 344, Application US/10159563  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Javed  
; APPLICANT: Ringner, Markus  
; APPLICANT: Peterson, Carsten  
; APPLICANT: Meltsar, Paul  
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR  
; CURRENT FILING DATE: 2002-12-09  
; PRIORITY APPLICATION NUMBER: US 10/133,937  
; PRIOR FILING DATE: 2002-04-25  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO: 344  
; LENGTH: 1646  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-10-159-563-344

Db 962 GGTGAACCTATGACCACTCATCAGGATGCCCTCGAAGGCCACCTCATGACAT 1021  
; Sequence 7, Application US/09884814  
; Patent No. US20020127600A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Jin-Iong  
; APPLICANT: Amaral, M. Catherine  
; APPLICANT: Tularik Inc.  
; TITLE OF INVENTION: Human Uncoupling Protein 2 (hUCP2): Compositions and  
; Methods of Use  
; FILE REFERENCE: 018781-001110US  
; CURRENT FILING DATE: 2001-05-18  
; PRIORITY APPLICATION NUMBER: US 09/884, 814  
; CURRENT FILING DATE: 2001-05-18  
; PRIORITY APPLICATION NUMBER: US 09/124, 293  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO: 7  
; LENGTH: 930  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURES:  
; NAME/KEY: CDS  
; LOCATION: (1)..(930)  
; OTHER INFORMATION: human uncoupling protein 2 (hUCP2), Fleury et al.  
; US-09-884-814-7

Query Match 38.6%; Score 475.6; DB 9; Length 930;  
Best Local Similarity 71.4%; Pred. No. 3.8e-129; Matches 673; Conservative 0; Mismatches 254; Indels 15; Gaps 3; Applicant: Khan, Javed  
Title of Invention: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS  
FILE REFERENCE: 11613\_56US11  
CURRENT FILING DATE: 2002-12-09  
PRIORITY APPLICATION NUMBER: US 10/159,563  
PRIOR FILING DATE: 2002-04-25  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: Patentin version 3.1

Db 61 GGCACACCTGCCTGATCAGATCTACCTTCTGATGATTCAGTCAGGCCCT 120  
; Sequence 344, Application US/10159563  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Javed  
; APPLICANT: Ringner, Markus  
; APPLICANT: Peterson, Carsten  
; APPLICANT: Meltsar, Paul  
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR  
; CURRENT FILING DATE: 2002-12-09  
; PRIORITY APPLICATION NUMBER: US 10/133,937  
; PRIOR FILING DATE: 2002-04-25  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO: 344  
; LENGTH: 1646  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-10-159-563-344

Db 274 CTCGAGTTCAGGGGGAACTCTGCTCCACATGAGATCTATGTCAGTGTGAGT 330  
; Sequence 344, Application US/10159563  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Javed  
; APPLICANT: Ringner, Markus  
; APPLICANT: Peterson, Carsten  
; APPLICANT: Meltsar, Paul  
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR  
; CURRENT FILING DATE: 2002-12-09  
; PRIORITY APPLICATION NUMBER: US 10/133,937  
; PRIOR FILING DATE: 2002-04-25  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO: 344  
; LENGTH: 1646  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-10-159-563-344

Db 181 GCTGTAGGCGCACATCTGACCATGCTGAGCTGAGGCGCCAGTCAGTCAGT 240  
; Sequence 344, Application US/10159563  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Javed  
; APPLICANT: Ringner, Markus  
; APPLICANT: Peterson, Carsten  
; APPLICANT: Meltsar, Paul  
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR  
; CURRENT FILING DATE: 2002-12-09  
; PRIORITY APPLICATION NUMBER: US 10/133,937  
; PRIOR FILING DATE: 2002-04-25  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO: 344  
; LENGTH: 1646  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-10-159-563-344

Db 391 GGCCTGGCGGGCTGCAAGGGCAAGTGAATGAGCTTCCTCATGGCATGGCTCT 450  
; Sequence 344, Application US/10159563  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Javed  
; APPLICANT: Ringner, Markus  
; APPLICANT: Peterson, Carsten  
; APPLICANT: Meltsar, Paul  
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR  
; CURRENT FILING DATE: 2002-12-09  
; PRIORITY APPLICATION NUMBER: US 10/133,937  
; PRIOR FILING DATE: 2002-04-25  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO: 344  
; LENGTH: 1646  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-10-159-563-344

Db 241 GGCTGTTGGCGGGCTGCAAGGGCAAGTGAATGAGCTTCCTCATGGCATGGCTCT 300  
; Sequence 344, Application US/10159563  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Javed  
; APPLICANT: Ringner, Markus  
; APPLICANT: Peterson, Carsten  
; APPLICANT: Meltsar, Paul  
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR  
; CURRENT FILING DATE: 2002-12-09  
; PRIORITY APPLICATION NUMBER: US 10/133,937  
; PRIOR FILING DATE: 2002-04-25  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO: 344  
; LENGTH: 1646  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-10-159-563-344

OTHER INFORMATION: Source, typically mammalian, most typically human

QY

451 GACTCGTCAGGAGGTGACACCCCAAGGGGGACAACCTCAGGCCCTCATCCCCG 510

Db

301 GATTCTGTCATAAACAGTCTACA--CCAGCGCTCTGAGCATGCCAGATGGAGCCG 357

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511 ATTTGGCCGAGCTGCACAGGAGCATGGGTGACTCTGCCCAGGCCAAGATG 570

Db

358 CTCTCTAGAGGCCAGGCCAGTGCGTGGTGGCTGGCTGGCTGGCTGGCTGG 417

OY

571 GTGAAGGTCCGATTAGGGAGCATACCTGGGACCATCGAGGCAAGAAATC 630

Db

418 GTAAAGTCCGATTCAGCAGC-----TCAGGCGGGCTGGGTGAGGATAC 468

OY

631 AGGGGAGACTGAGGAGCTACAGAACCTGGCCAGGGAGAAGTCAGGGCTGG 690

Db

469 CAAGGACCGTCAATGCTAGAGACCATGCCCAGAGGGTCCGGCTCTGG 528

OY

691 AAAGGAACTTGGCCACATCATGAGGAATCTATCGTCAACTTCCTGGTGAAC 750

Db

529 AAAGGACACTCTCCATGTTGCTGTAATGCCATGAGGAACTTCCTGGTGAAC 588

OY

751 TAGACATCCCTAAAGGAAGCTGCTGAGCTACCCACTGCTGACTGACAAC 810

Db

589 TAGACCTCATCAAGATGCCCTCTGAAAGCCACCTCATGAGATGACCTCC 648

OY

811 CACTTGCTCTGCTGAGGAGCTGCTGAGCTGCTGAGCTGCTGAGCTGCTG 870

Db

649 CACTCATTCCTGCCTTGCGGAGCTCTGACCATCTGTCATCCCTGAGAC 708

OY

871 GTGGTGAAGCCGGTATAGACTCACCTCCACGGCAGTACTTCAGCCCTGACT 930

Db

709 GTGGTCAAGAGAGATACATGACTGCTGCTGGCCAGTAAAGTACACCTCC 970

OY

931 ATGATAAAGATGGTGGCCAGGAG3GCCAACAGCTCTAACAGGGATTACACCTC 990

Db

769 GCCTTACCATCTCCAGAGGGGGCCGGCTTCAGAAGGTTCTACGGTCTCC 828

OY

991 TTTCGCGTGGGATCTGAACTGCTGTTGTAACCTATGAGCAGTGAAACGG 1050

Db

829 TTTCGCGTGGTCTGGACAGCTGGTGTGTTGTCACCTATGAGCAGTGAAACGA 888

OY

1051 GCCCTGATGAAGTCAGATCTACGGGATCACCGTTGA 1092

Db

889 GCCTCATGCGCTGCACTTCCCAGAGGACTCCCTCTGA 930

RESULT 14

US-10-001-051B-1

sequence 1, Application US/10001051B

GENERAL INFORMATION:

APPLICANT: Gonzalez-Zulueta, Mirella

APPLICANT: Shamloo, Mehrdad

APPLICANT: McFarland, K.C.

APPLICANT: Chin, Daniel

APPLICANT: Wieloch, Tadeusz

APPLICANT: Melcher, Thorsten

APPLICANT: AGY Therapeutic, Inc.

TITLE OF INVENTION: METHODS OF DIAGNOSING, PREVENTING AND TREATING

FILE REFERENCE: 019488-003010US

CURRENT FILING DATE: 2002-06-25

PRIOR APPLICATION NUMBER: US 60/244,946

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin Ver. 2.1

LENGTH: 930

TYPE: DNA

FEATURE: Unknown Organism

OTHER INFORMATION: Description of Unknown Organism: Any animal

RESULT 15



GenCore version 5.1.6  
(c) 1993 - 2004 Compugen Ltd.

AK054060 Mus muscu  
AK035298 Mus muscu  
AY413339 Mus muscu

Run on: May 18, 2004, 11:18:36 ; Search time 3063 Seconds  
OM nucleic - nucleic search, using sw model  
(without alignment)

12001.418 Million cell updates/sec

**Title:** US-09-423-410-3  
**Perfect score:** 1231  
**Sequence:** tccttggatggcccttaagg.....ttgttgtgtgttcagaac 1231

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Searched: **27513289 seqB**, 14931090276 residues  
Searched: **27513289 seqB**, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

**Post-processing:** Minimum Match 0% Maximum Match 100%

Database : RSM.\* listing first 45 summaries

1: em-estba:  
2: em-esbhum:\*

3: em\_eastin: \*  
4: em\_eastmu: \*  
5: em\_eastov: \*

6: em\_estrpl:  
7: em\_estrto:  
8: em\_estrta:

6: **err\_nuc:**  
9: **gb\_est1:\***  
10: **gb\_est2:\***

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11: 9b_htca:*
12: 9b_est3:*
13: 9b_eat4:*
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14: gb_best5:*
15: em_estfun:*
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16: em\_g88\_em:  
17: em\_g88\_hum:  
18: em\_g88\_inv:\*

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19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fim:*
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22: em_gss_mam:*
23: em_gss_mub:*
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24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_pha:*
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27: em_gss_vrl:*
28: gb_gss1:*
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Pred. No. is the number of results predicted by chance to

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	939	76.3	939	29	AY06944	AY06944 Homo sapi
2	680.6	55.3	927	29	AY06946	AY06946 Mus muscu
3	611.2	49.7	808	13	BUT45943	BUT45943 CH2#003_H
4	595.6	48.4	602	29	AY06945	AY06945 Pan trogl

DEFINITION	Homo sapiens UCP3 gene, VIRTUAL TRANSCRIPT, partial sequence,
ACCESSION	AY06944
VERSION	AY06944.1
KEYWORDS	GSS.
ORGANISM	Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (bases 1 to 919)
AUTHORS	Todd, M.A., Gitanjali, S., Nielson, R., Thomas, P., Kejariwal, A., Clark, A.G., Gitanjali, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanebaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
TITLE	Inferred nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL	Science 302 (5652), 1960-1963 (2003)
PUBLISHED	14/07/2002
PERCENT DIFFERENCE	2 (bases 1 to 939)
AUTHORS	Clark, A.G., Gitanjali, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanebaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
TITLE	Direct submission

JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES source	<p>1. .-939</p> <p>/organism="Homo sapiens"</p> <p>/mol_type="genomic DNA"</p> <p>/db_xref="taxon:9606"</p> <p>&lt;1.-&gt;939</p> <p>/gene="UCP3"</p> <p>/locus_tag="HCM2726"</p>
ORIGIN	
Query Match	76.3%; Score 939; DB 29; Length 939;
Best Local Similarity	100.0%; Pred No. 7.5e-200;
Matches	939; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	154 ATGGTGTGACTGAAAGCTTCAGACGTCCTCCACATGGTGAGTTCTGGGCA 213
Db	1 ATGGTGTGACTGAAAGCTTCAGACGTCCTCCACATGGTGAGTTCTGGGCA 60
Qy	214 CGCACCGAGCTGTTGCTGACCTGTTACCTTCCACTGGACACAGCAGGTCGC 273
Db	61 GGCACCGAGCTGTTGCTGACCTGTTACCTTCCACTGGACACAGCAGGTCGC 273
Qy	274 CTGAGATCCGGGAGAACAGGGCTCTAGGACCTACCCGATCTGGGC 333
Db	121 CTGAGATCCGGGAGAACAGGGCTCTAGGACCTACCCGATCTGGGC 180
Qy	334 CTGGCTGGCACATCCAGACATGGGGGAGCTGGGCTCTGGAGCCCTACATGG 393
Db	181 CTGGCTGGCACATCCAGACATGGGGGAGCTGGGCTCTGGAGCCCTACATGG 240
Qy	394 CTGGTGGCGGCGCTGCGGGCGAGTAGCTGGCTCGCTCCATCGGATCGGC 453
Db	241 CTGGTGGCGGCGCTGCGGGCGAGTAGCTGGCTCGCTCCATCGGATCGGC 300
Qy	454 TCGTCAAGCAGGTGTACACCCCAAAGGCGCGAACACTCAGCCCTACTACCGATT 513
Db	301 TCGTCAAGCAGGTGTACACCCCAAAGGCGCGAACACTCAGCCCTACTACCGATT 360
Qy	514 TGGCGCGACTACCAACAGGGCGTGGCGTGGCGGCCAGCGAGATGGTG 573
Db	361 TGGCGCGCTACCAACAGGGCGTGGCGTGGCGGCCAGCGAGATGGTG 420
Qy	574 AAGTCGATTTCAGCCAGGATACCTCGGCCATCCAGGAGCGAGAAATACAGC 633
Db	421 AAGTCGATTTCAGCCAGGATACCTCGGCCATCCAGGAGCGAGAAATACAGC 480
Qy	634 CGGACTATGGAGCCTACAGAACCATGGCGGAGGAGAGCTGGGCTGTGAAA 693
Db	481 CGGACTATGGAGCCTACAGAACCATGGCGGAGGAGAGCTGGGCTGTGAAA 540
Qy	694 CGGACTTGCCTACATGAGGAATGCTATGTCACACTGGCTGGAGTTGACCTAC 753
Db	541 CGGACTTGCCTACATGAGGAATGCTATGTCACACTGGCTGGAGTTGACCTAC 600
Qy	754 GACATCTCAAGGAGAACCTGGACTACACCTGTCACAGAACCTCCCTCAC 813
Db	601 GACATCTCAAGGAGAACCTGGACTACACCTGTCACAGAACCTCCCTCAC 660
Qy	814 TTGTCTCTGCCCTGGAGCGCGCTCTGGCAACAGTGGGCTCCCGGGTGGAGT 873
Db	661 TTGTCTCTGCCCTGGAGCGCGCTCTGGCAACAGTGGGCTCCCGGGTGGAGT 720
Qy	874 GTCAGAAGCCGGATATGAACTACCTCGGCCAGACTGACTGACCTCTCACTGAG 933
Db	721 GTGAGAGCCGGATATGAACTACCTCGGCCAGACTGACTGACCTCTCACTGAG 780
Qy	934 ATTAAGTGTGCCCAAGGAGGCCCAAGCTTCTCAAGGATTACACCTCCCT 993
Db	781 ATTAAGTGTGCCCAAGGAGGCCCAAGCTTCTCAAGGATTACACCTCCCT 840
RESULT 2	
LOCUS	AY406946
DEFINITION	Mus musculus UCP3 gene, VIRTUAL TRANSCRIPT, partial sequence,
ACCESSION	AY406946
VERSION	AY406946.1
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Mus musculus (house mouse)
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 927)
AUTHORS	Clark,A.G., Gianoowski,S., Nielsen,R., Thomas,P., Kejariwal,A., Todd,M.A., Tennenbaum,D.M., Civeillo,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Srinivas,Y.J., Adams,M.D. and Cargill,M.
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL	Science 302 (5652), 1960-1963 (2003)
PUBLISHED	16/7/2002
REFERENCE	(bases 1 to 927)
AUTHORS	Clark,A.G., Gianoowski,S., Nielsen,R., Thomas,P., Kejariwal,A., Todd,M.A., Tennenbaum,D.M., Civeillo,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Srinivas,Y.J., Adams,M.D. and Cargill,M.
TITLE	Direct Submission
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES source	<p>1. .-927</p> <p>/organism="Mus musculus"</p> <p>/mol_type="genomic DNA"</p> <p>/db_xref="taxon:10090"</p> <p>&lt;1.-&gt;927</p> <p>/gene="UCP3"</p> <p>/locus_tag="HCM2726"</p>
ORIGIN	
Query Match	55.3%; Score 680.6; DB 29; Length 927;
Best Local Similarity	84.5%; Pred No. 7.2e-142;
Matches	793; Conservative 0; Mismatches 134; Indels 12; Gaps 2;
Qy	154 ATGGTGTGACTGAAAGCTTCAGACGTCCTCCACATGGCTGGAGTTCTGGGGCA 213
Db	1 ATGGTGTGACTGAAAGCTTCAGACGTCCTCCACATGGCTGGAGTTCTGGGGCA 60
Qy	214 CGCACCGAGCTGTTGCTGACCTGTTACCTTCACAGGACAGGAGGTCGC 273
Db	61 GGCACCGAGCTGTTGCTGACCTGTTACCTTCACAGGACAGGAGGTCGC 120
Qy	274 CTGAGATCCGGGAGAACAGGGCTCTAGGACCGCCGGCTCTGCACTCTGGC 333
Db	121 CTGAGATCCGGGAGAACAGGGCTCTAGGACCGCCGGCTCTGCACTCTGGC 171
Qy	334 CTGGCTGGCACATCTGACCTGGGGACTGAGGGTCTCTGGAGCCCTACAGGG 393
Db	172 CTGGCTGGTACCATCTGACCTGGGGACTGAGGGTCTCTGGAGCCCTACAGGG 231
Qy	394 CTGGCTGGCACATCTGACCTGGGGACTGAGGGTCTCTGGAGCCCTACAGGG 453

Db	232 CTGGCGCTGCTGACCCGCCAGATGAGTTTGCTCCATTGAAATTGGCTCTAACGAC 291	FEATURES	High quality sequence stop: 637.
Qy	454 TCGTCAGCAGGTACACCCCAAGGCCGAACTCACTTCACTGGATT 513	source	Location/Qualifiers
Db	292 TCTGTCAGCAGGTCTCACCCCAAGGCCGAACTCACTTCACTGGATT 351	/organism="Canis familiaris" /mol_type="mRNA" /db_xref="ttaxon:9615" /clone="CH2#03_H04"	
Qy	514 TTGGCGCTGCTGACCCAGGAGGCACTGGCTGACCTGGCCATCCAGGAGCAGAAATACAGC 573	/tissue="Organ: heart" /cell_type="heart" /dev_stage="mixed developmental stages (adult, 30 day - 40 day fetal)" /clone lib="Canine heart normalized cDNA library in pBlueScript" /note="Organ: heart; Vector: pBlueScript; Site_1: 5' of vector NotI; Site_2: 3' of vector BclRI; tissue source: dog heart (adult, 30 day - 40 day fetal), right and left atria and ventricle. Dog breed - mixed (beagle, German shepherd, pointer, Irish setter). Library construction: oligo-dT primed"	
Db	352 CTGGCGCTGCTGACCCAGGAGGCACTGGCTGACCTGGCCATCCAGGAGCAGAAATACAGC 411		
Qy	574 AAGGTCGATTTCAGGCGCATACACCTCGCCATCCAGGAGCAGAAATACAGC 633		
Db	412 AAGGTCGATTTCAGGCGCATACACCTCGCCATCCAGGAGCAGAAATACAGC 468		
Qy	634 GGAGACTATGGACCCATACAGAACCTTGCCAGGGAGAAGGTAGGGGCTTGGAAGA 693		
Db	469 GGAGACTATGGACCCATACAGAACCTTGCCAGGGAGAAGGTAGGGGCTTGGAAGA 528		
Qy	694 GGAGACTTGCACACATGAGGAATGCTTGTCACTTGCTAGGGTGTGACTAC 753		
Db	529 GGAGACTTGCACACATGAGGAATGCTTGTCACTTGCTAGGGTGTGACTAC 588		
Qy	754 GACATCCTCAAGGAGAGCTCTGGACTACCTCCCTCTCACTGACACTTCCCCTCCAC 813		
Db	589 GACATCCTCAAGGAGAGCTCTGGACTACCTCCCTCTCACTGACACTTCCCCTCCAC 648		
Qy	814 TTGTCTCTGACTTGTGAGCGCTCTGTCACAGTGGCCCTGGAGCTG 873		
Db	649 TTGTCTCTGACTTGTGAGCTGCTGTCAGTGGCCCTGGAGCTG 708		
Qy	874 CTGAGAGCCGGTATACTGAACTTACCTCCCTAGCAGGCTCTGACTATG 933		
Db	709 GTAAAGAGCCGATACATGAACTTACCTCCCTAGCAGGCTCTGACTATG 768		
Qy	934 ATAAAGATGGCCGCCAGGAGGCCAACAGGCTCTAACCTCTT 993		
Db	769 CTGAGAGCTGTCCTCTGAGGAGACCCTGGCTCTAACAGGATTG 828		
Qy	994 TTGGTTGGATCTCGAACTGGTGTGTAACCTATGAGGCTGAAACGGCC 1053		
Db	829 CTGGGTTGGAGCTTGAACTGTGATTTGTGATCATATGAGCACTGAGAGGCC 888		
Qy	1054 CTGATGAAAGTCAGATGTTAGGGATCACCGTTGA 1092		
Db	889 TTAATGAAAGTCAGGACTCTGGGAATCTCGTTGA 927		
<b>RESULT 3</b>			
BUT45943	BUT45943 808 bp mRNA Linear EST 10-OCT-2002		
DEFINITION	CH2#003_H04T7 Canine heart normalized cDNA library in pBluescript		
CANIS	Canis familiaris cDNA clone CH2#003_H04 5', mRNA sequence.		
VERSION	BUT45943		
KEYWORDS	BUT45943.1 GI:2365606		
SOURCE	EST: BUT45943		
ORGANISM	Canis familiaris (dog)		
Bukreyova, Meirzaa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Carnivora; Fissipedia; Canidae; Canis.			
REFERENCE	1 (bases 1 to 808)		
AUTHORS	Yi, Y., Desai, R., Olarte, M., Henthorn, P. and George A.L.		
JOURNAL	Expressed sequence tags from Canine heart		
COMMENT	Unpublished (2003)		
Vanderbilt University	Division of Genetic Medicine		
Vanderbilt University	529 Light Hall, 2215 Garland Avenue, Nashville, TN 37232-0275, USA		
Tel:	615 936 2661		
Fax:	615 936 2661		
Email:	al.george@vanderbilt.edu		
Insert length:	1782	Seq Error:	0.00
Seq primer:	T7: TAATACGACTCACTATCG		
High quality sequence start: 40			

Qy	1029	ACCTATGAGGCTAACGGCCCTGATTAAGTCAGTGTAGGGAAATCAGCTT	1088	Qy	791	TCACTGACAACCTCCCCGACACTTGCTCTGCCATTGGAGCCAGCTCTGTGCCACAG	850
Db	738	GACCTATGAGGCTAACGGCCCTGATTAAGTCAGTGTAGGGAAATCAGCTT	797	Db	301	TCACTGACAACCTCCCCGACACTTGCTCTGCCATTGGAGCCAGCTCTGTGCCACAG	360
Qy	1089	TGAACTAGAG 1097		Qy	851	TGGTGCCTCCCGCTGAGCTGTGAGAAGCCGCTATATGAACTCAGCTCCAGGCAAGT	910
Db	798	CTGAAGTAG 806		Db	361	TGGTGCCTCCCGCTGAGCTGTGAGAAGCCGCTATATGAACTCAGCTCCAGGCAAGT	420
RESULT 4				Qy	911	ACTTCAGCCCTGACTGTATAAGATGGTGCCAGGAGGCCACAGCTCT	480
AY405945	AY405945	Pan troglodytes UCP3 gene, VIRTUAL TRANSCRIPT, partial sequence,	602 bp	DNA	421	ACTTCAGCCCTGACTGTATAAGATGGTGCCAGGAGGCCACAGCTCT	970
LOCUS		genomic survey sequence.		DEFINITION	971	ACAAGGGATTACACCCCTTTGGTTGGATCTGGAGACGTGGATGTCGAA	1030
ACCESSION		AY06945		ACCESSION	481	ACAAGGGATTACACCCCTTTGGTTGGATCTGGAGACGTGGATGTCGAA	540
VERSION		AY06945.1		VERSION	1031	CCTATGAGCAGCTGAAACGAGGCCCTGATGAAAGTCAGATGTTACGGAAATCACGGTT	1090
KEYWORDS		GSS.		KEYWORDS	541	CCTATGAGCAGCTGAAACGAGGCCCTGATGAAAGTCAGATGTTACGGAAATCACGGTT	600
SOURCE		Pan troglodytes (chimpanzee)		SOURCE	1091	GA	1092
ORGANISM		Pan troglodytes		ORGANISM	601	GA	602
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;		REFERENCE			
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.		AUTHORS			
1	{bases 1 to 602}	Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Torenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J., Adams,M.D. and Cargill,M.		1			
TITLE		Direct Submission		TITLE			
JOURNAL		Submitted (16-Nov-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA		JOURNAL			
COMMENT		This sequence was made by sequencing genomic exons and ordering them based on alignment/Qualifiers		COMMENT			
FEATURES		Location/Qualifiers		FEATURES			
source		1..602		source			
ORIGIN		/organism="Pan troglodytes"		ORIGIN			
Query Match	48.4%	Score 595.6; DB 29; Length 602;		Query Match	42.2%	Score 519.2; DB 9; Length 613;	
Best Local Similarity	99.3%	Pred. No. 7e-123; Mismatches 598; Conservative 0; Indels 0; Gaps 0;		Best Local Similarity	99.3%	Pred. No. 9.9e-106; Mismatches 532; Conservative 0; Indels 1; Gaps 1;	
Matches				Matches			
Qy	491	ACTCCAGGCTACTACCGGATTGGCGGCTGACCGACGGCATGCGGTTGACT	550	Qy	611	CCGAGGAGGAGAGAAATACGGGGATACTGGACGCTAACAGAACCTGGGG	670
Db	1	ACTCCAGGCTACTACCGGATTGGCGGCTGACCGACGGCATGCGGTTGACT	610	Db	121	CCGAGGAGGAGAGAAATACGGGGATACTGGACGCTAACAGAACCTGGGG	180
Qy	551	GTCGCCAGCCACAGATGTTGGAGGCTGAGCTGGGGCTGACCGACGGCAT	610	Qy	61	GTCGCCAGCCACAGATGTTGGAGGCTGAGCTGGGGCTGACCGACGGCAT	120
Db	61	GTCGCCAGCCACAGATGTTGGAGGCTGAGCTGGGGCTGACCGACGGCAT	60	Db	61	GTCGCCAGCCACAGATGTTGGAGGCTGAGCTGGGGCTGACCGACGGCAT	60
Qy	611	CCGAGGAGGAGAGAAATACGGGGATACTGGACGCTAACAGAACCTGGGG	670	Qy	611	CCGAGGAGGAGAGAAATACGGGGATACTGGACGCTAACAGAACCTGGGG	670
Db	121	CCGAGGAGGAGAGAAATACGGGGATACTGGACGCTAACAGAACCTGGGG	180	Db	121	CCGAGGAGGAGAGAAATACGGGGATACTGGACGCTAACAGAACCTGGGG	180
Qy	671	AAGGAGTCAAGGGCTGTCGAAAGGAACCTTGCCAAACATCAGGAGATGTGCA	730	Qy	671	AAGGAGTCAAGGGCTGTCGAAAGGAACCTTGCCAAACATCAGGAGATGTGCA	730
Db	181	AAGGAGTCAAGGGCTGTCGAAAGGAACCTTGCCAAACATCAGGAGATGTGCA	240	Db	181	AAGGAGTCAAGGGCTGTCGAAAGGAACCTTGCCAAACATCAGGAGATGTGCA	240
Qy	731	ACTGTGCTGAGGCTGAGCTACACATCTCAGGAGAGCTTGACTACACTGC	790	Qy	731	ACTGTGCTGAGGCTGAGCTACACATCTCAGGAGAGCTTGACTACACTGC	300
Db	241	ACTGTGCTGAGGCTGAGCTACACATCTCAGGAGAGCTTGACTACACTGC	300	Db	241	ACTGTGCTGAGGCTGAGCTACACATCTCAGGAGAGCTTGACTACACTGC	300
ORIGIN				ORIGIN			
Query Match	42.2%	Score 519.2; DB 9; Length 613;		Query Match	42.2%	Score 519.2; DB 9; Length 613;	
Best Local Similarity	99.3%	Pred. No. 9.9e-106; Mismatches 532; Conservative 0; Indels 1; Gaps 1;		Best Local Similarity	99.3%	Pred. No. 9.9e-106; Mismatches 532; Conservative 0; Indels 1; Gaps 1;	
Matches				Matches			

OY	1 TCTGGGATGCGAACCCCTAGGGAAACCCGTGCTTGCAGCTACAGCC	60	JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
Db	78 TCTGGGATGCGAACCCCTAGGGAAACCCGTGCTTGCAGCTACAGCC	137	JOURNAL	20530913
Db	61 CCACCCGTCACTGAGGCCAGGGTGTGAGCAGCTCTCCGAGGACTCAAGCC	120	PUBLMED	11076861
QY	138 CCACCGTCACTGAGGCCAGGGTGTGAGCAGCTCTCCGAGGACTCAAGCC	197	REFERENCE	4
Db	121 CCTAAAGGAAGCTGGAGGCTTCAGGACTATGGTGGACTGAGCTTCAGCTTG	180	REFERENCE	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
QY	198 CCTAAAGGAAGCTGGAGGACTGGCAGACCTCTGAGCTCTCCGAGGACTCAAGCC	257	AUTHORS	National annotation of a full-length mouse cDNA collection
QY	181 CCTCCACCATGCGTGTGAGTTCTCTGGGAGGACAGGACAGGCTGTTTGCTGACCTC	240	TITLE	Functional annotation of a full-length mouse cDNA collection
Db	258 CCTCCACCATGCGTGTGAGTTCTCTGGGAGGACAGGACAGGCTGTTTGCTGACCTC	317	JOURNAL	Nature 409, 685-690 (2001)
QY	241 GTTACCTTCACAGCACGCCAGGTCGGCTCAGATCAGGGGAAACAGGG	300	REFERENCE	5
Db	318 GTTACCTTCACAGCACGCCAGGTCGGCTCAGATCAGGGGAAACAGGG	377	AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
QY	301 GTCAGAGGCCGGCTCGTCAGTACCGTGGCTCTGAGGACCATCTGAGCCATGGG	360	TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Db	378 GTCCAGACGGCCCGCTCGTCAGTACCGTGGCTCTGAGGACCATCTGAGCCATGGG	437	JOURNAL	Nature 420, 563-573 (2002)
QY	361 CGGACTGAGGTCCTCTGAGCCCTAACGGTGTGAGGCTGAGGCGCTGAGGCCGATG	420	REFERENCE	6 (bases 1 to 3641)
Db	438 CGGACTGAGGTCCTCTGAGCCCTAACGGTGTGAGGCTGAGGCGCTGAGGCCGATG	497	AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hangaki, T., Hara, A., Hashizume, W., Hayashizaki, Y., Horii, P., Imotani, K., Ishii, Y., Itoh, M., Kawano, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, M., Hirozane, T., Koyama, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakzume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Tomaru, T., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
QY	421 ACTGGCCCTCCATCGCATGGCTCTATGAC-TGGTCAAGGGTGTGACCCCCAA	479	TITLE	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, fax: 81-45-503-9216)
Db	498 AGGGGGGACACTCCAGCTTCAACCGGATTGGCCGCGCTGACCAAGGG	535	JOURNAL	CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
QY	558 AGGGGGGACACTCCAGCTTCAACCGGATTGGCCGCGCTGACCAAGGG	613	COMMENT	Please visit our web site for further details. URL: http://fantom.gsc.riken.go.jp/
RESULT	6		FEATURES	Location/Qualifiers
LOCUS	AK054060	3641 bp mRNA	source	I .. 3641
DEFINITION	Mus musculus 2 days pregnant adult female oviduct cDNA, RIKEN full-length enriched library, clone:E230015118 product:uncoupling Protein 2, mitochondrial, full insert sequence.		/organism="Mus musculus"	
ACCESSION	AK054060		/mol_type="mRNA"	
VERSION	AK054060.1	GI:26343968	/strain="C57BL/6J"	
KEYWORDS	HPC; CAP trapper.		/db_xref="PANTOM DB:E230015118"	
SOURCE	Mus musculus (house mouse)		/db_xref="MGI:2425993"	
ORGANISM	Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Mus.		/db_xref="ttaxon:10090"	
REFERENCE	Carninci, P. and Hayashizaki, Y.		/clone="E230015118"	
AUTHORS	High-efficiency full-length cDNA cloning		/sex="female"	
TITLE	High-efficiency full-length cDNA cloning		/tissue_type="oviduct"	
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		/clone Lib="RIKEN full-length enriched mouse cDNA library"	
MEDLINE	99279253		/def_stage="2 days pregnant adult"	
POEMED	10349636		/protein_start=1	
REFERENCE	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		/protein_id="PAC35541_1"	
AUTHORS	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		/ab_xref="GI:26343699"	
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		/note="unnamed protein product; putative uncoupling protein 2, mitochondrial (MCP) [MGI:109354, GB_NM_011671, evidence: BLASTN, 100%, match:1100]"	
MEDLINE	2009374			
REFERENCE	Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Itoh, M., Kono, H., Okazaki, Y., Nakanura, S., Hazama, M., Nishine, T., Harada, A., Sumi, N., Ishii, Y., Nakamura, S., Hidai, T., Tashiro, H., Itoh, M., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Onara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuyura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.			
TITLE	RIKEN integrated sequence analysis (RISA) System--384-format		ORIGIN	Query Match
				39.8%; Score 489.4; DB 11; Length 3641;



FEATURES	URL: <a href="http://genome.gsc.riken.go.jp/">http://genome.gsc.riken.go.jp/</a> .	
source	Location/Qualifiers	
	1. 3964 /organism="Mus musculus" /mol_type="mRNA" /clone="C7BL/6U" /db_xref="PANTOM DB:9530011110" /ab_xref="NCI:2399541" /db_xref="taxon:10090" /clone="9530011110" /sex="male"	
	/tissue_type="urinary bladder" /clone_id="RIKEN full-length enriched mouse cDNA library" /dev_stage="adult" /note="unnamed protein product; putative uncoupling protein 2, mitochondrial (MGI:MGI:109354, GR:NM_011671, evidence: BLASTN, 100%, match=1100)" /codon_start=1 /protein_id="BAC29201.1" /db_xref="GR:26330582" /translation="MVGKAKATDVPTATVKFOGAGTAAACIAIDLTPDIAKURLOQ GRSQGLVTRTAASQYRGFTLTMVRGFTLWVQPLVYKVRIOAQARQMFASVRGLYLVY VKQFYTQKGSEHAGIGSISLAGSTGALAVAVQPTDVYKVRIOAQARQMFASVRGLYLVY EAKTIKABEGRGLWKETSPVARNVINCALVTLIUKOTLUKANLMDDLPCH TSAFGKAFCTTVIASPODVVKYTMNSLQWVHSAGHCALTMLRKEGRAFYKGFMPS FRLGSMNNVMFVTFYEQDQLRNLAYQSOEARPE"	
ORIGIN		
Query Match	39.6%: Score 487.8; DB 11; Length 3964;	
Best Local Similarity	71.9%; Pred. No. 2.6e-98;	
Matches	684; Conservative 0; Mismatches 252; Indels 15; Gaps 3;	
QY	147 CAGGCTAAGTTGACTGAAGCCCTCACAGCTGAGCTGCTCCACCAAGGGCTGTGAGTTCT 205	
Dp	356 CAGAATCATGGTTCTTCAGGCCAACAGCACTGAGCTGACCTTCA 415	
QY	207 GGGGCGAGGCACAGGAGCCCTGTTCTGACTCTGTTACCTTCACTGGACACGCCA 266	
Dp	416 GGAGCTCTGGCACAGCTGCGCTGAGTCATCTCATCTTCTGCTGATACGCCAA 475	
QY	267 GTTCCGCGCTTCAGATTCAGGGGAGAACCAAGGGCG--GTCGAGAGGGCCGCTGTGCA 323	
Dp	476 GGTCCGGCTTCAGATTCAGGGGAGAACCACTCTGACATGTTGGGCTGCTGAGGCCA 535	
QY	324 GTACCGTGAGCTTCCTGGTACCATCTAACATGGGGCTGAGGTACGGTACGGTACGGCTCACGGAGCT 595	
Dp	536 GTACCGTGAGCTTCCTGGTACCATCTAACATGGGGCTGAGGTACGGTACGGCTCACGGAGCT 595	
QY	384 CTACCATGGCTGGCCGCCCTGAGGGCTGGCTCATCCGGATCG 443	
Dp	596 CTACCATGGCTGGCCGCCCTGAGGGCTGGCTCATCCGGATCG 655	
QY	444 CCTCTATGACTCCGGCAAGCAGGTTCATAACCCCCAACGGGGGAACTCCAGGCTCAC 503	
Dp	656 CCTCTATGACTCTGTCACAGTCCTACA --CCAGGCTCAGACATGGAGCTCG 712	
QY	504 TACCGGATTTCGGGGCTGACCAAGGAGCTGGCTGACTGTGCCAACCCAC 563	
Dp	713 GAGCCGCTCTGGAGGAGCTACCAACAGGGCTGGCTGGTGTAGCCACCTAC 772	
QY	564 AGATCTGGAGGGCGATTCAGCCAGGATAACCTCGGCCATCCAGGAGACAG 623	
Dp	773 AGATCTGGTAAAGGTCGCTTCAGGC-----TCAGGCCGGCTGCTGGTGTG 823	
QY	624 AAAATACAGGGGATATGGAGGCTACAGAACCTGGCTGGGAGGGTCAAGGG 683	
Dp	824 GAGATACAGGAGCTCTGCAAGCTACAGAACCTGGCTGGGAGGGTCAAGGG 883	
QY	684 CCTGGGAAGGAACTTGTCCAAACATCATGAGGAATGCTATGTCACATGCTGTGAGT 743	
Dp	884 CCTCTGGAAAGGAGCTCTCCAAAGTGTCCGGTGTGCAATGTGCTGTGAGCT 943	
ORIGIN		
Query Match	39.5%: Score 486.8; DB 29; Length 930;	
Best Local Similarity	72.4%; Pred. No. 2.2e-98;	
Matches	680; Conservative 0; Mismatches 247; Indels 15; Gaps 3;	
QY	154 ATGGTGGACTGAGGCTTCAGCGCTCCACCATGGCTGTGAACTTCTGGGSCA 213	
RESULT 8		
LOCUS	AY413339	
DEFINITION	930 bp DNA linear transcript, partial sequence.	
ACCESSION	AY413339	
VERSION	AY413339.1	
KEYWORDS	GI:39769301	
SOURCE	GSS.	
ORGANISM	Mus musculus (house mouse)	
REFERENCE	Bularyota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
AUTHORS	1 (bases 1 to 930) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tenenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J., Adams,M.D. and Caggil,M.	
TITLE	Inferred nonneutral evolution from human-chimp-mouse orthologous gene trios	
JOURNAL	Science 302 (5652), 1960-1963 (2003)	
PUBLISHED	14571302	
REFERENCE	2 (bases 1 to 930) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tenenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J., Adams,M.D. and Caggil,M.	
AUTHORS	Direct Submission	
TITLE	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA	
JOURNAL	COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES	Location/Qualifiers	
source	1. 930 /organism="Mus musculus" /mol_type="Genomic DNA" /db_xref="taxon:10090" <1->930 /gene="UCG2" /locus_tag="HCM4857"	
ORIGIN		
Query Match	39.5%: Score 486.8; DB 29; Length 930;	
Best Local Similarity	72.4%; Pred. No. 2.2e-98;	
Matches	680; Conservative 0; Mismatches 247; Indels 15; Gaps 3;	
QY	154 ATGGTGGACTGAGGCTTCAGCGCTCCACCATGGCTGTGAACTTCTGGGSCA 213	

Db	1	ATGGTGGTTAACGCCACGATGCCCAACGCCACTGAGCTCTGGGCT	60	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Qy	214	GGCACAGCAGCCTGTTGTGACCTTGTCATCCAGGACACCGAAGTCCG	273	REFERENCE AUTHORS 1 (bases 1 to 930)
Db	61	GGGACAGCTGCTGCATGCACTCATCTTCTCTGGATACCGCCAGTCGG	120	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kjariwal,A., Todd,M.A., Tenenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Srinivas,Y.J.J., Adams,M.D. and Cargill,M.
Qy	274	CTGCAGATCCGGGGAGAGCAGGG--GTCGAGGGCCGCTGCGAGCT	330	inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
Db	121	CTGCAGATCCGGGGAGAGCAGGG--GTCGAGGGCCGCTGCGAGCT	180	Science, 302 (5652), 1960-1963 (2003)
Qy	331	GGCGTCTGCCCCACCATCTCTTACCCCTGCTGAGCTGGCTAGCGT	390	JOURNAL PUBLMED 14671302 (bases 1 to 930)
Db	181	GGCGTCTGCCCCACCATCTCTTACCCCTGCTGAGCTGGCTAGCGT	240	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kjariwal,A., Todd,M.A., Tenenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Srinivas,Y.J.J., Adams,M.D. and Cargill,M.
Qy	391	GGCGTCTGCCCCACCATCTCTTACCCCTGCTGAGCTGGCTAGCGT	450	Direct Submission
Db	241	GGCGTCTGCCCCACCATCTCTTACCCCTGCTGAGCTGGCTAGCGT	300	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
Qy	451	GACTCTGCTAACGAGGTAAACCCCACACGGGACACTCCACCTTAC	510	This sequence was made by sequencing genomic exons and ordering them based on alignment.
Db	301	GACTCTGCTAACGAGGTAAACCCCACACGGGACACTCCACCTTAC	357	Location/Qualifiers 1..930
Qy	511	ATTGGCGGCTGACCGAGGCTGGGGTACGCCACAGATGTG	570	/organism="Homo sapiens" (/mol_type="genomic DNA" <db_xref="taxon:9606" /gene="UCP2" /locus_tag="HCM4857"
Db	358	CTCTGAGCTGAGCTGACCGAGGCTGGGGTACGCCACAGATGTG	417	FEATURES SOURCE
Qy	571	GTGAAGCTCCATTGCGGAGCATACCTCGGCCATCGAGGAGAAATAC	630	COMMENT Best Local Similarity 38.5%; Score 474; DB 29; Length 930; Matches 672; Conservative 0; Mismatches 255; Indels 15; Gaps 3;
Db	418	GTAAAGCTCCATTGCGGAGCATACCTCGGCCATCGAGGAGAAATAC	468	Query Match 1 ATGGTGGTTAACGCCACGATGCCCAACCTGGGCT
Qy	631	ACGGGACTATGAGCTGAAACATCGAGGAGGAGTCAGGGCTG	690	1 ATGGTGGTTAACGCCACGATGCCCAACCTGGGCT
Db	469	CAGAGCACTGCTGAAACATCGAGGAGGAGTCAGGGCTG	528	214 GGCACAGCAGCCTGTTGTGACCTTGTCATCCAGGACAGTCGG
Qy	691	AAAGGAACTTCCACATCTGAGGAGATCTATGCACTGTTGAGGTGACC	750	61 GGCAACAGCTCTGCACTGCACTGAGCTCATCTACCTTCTCTGATACTGCAAGTCGG
Db	529	AAAGGAACTTCCACATCTGAGGAGATCTATGCACTGTTGAGGTGACC	588	870 1 ATGGTGGTTAACGCCACGATGCCCAACCTGGGCT
Qy	751	TAGACATCTCCATGAGGAACTGAGCTACCACTGTCATCCCTG	810	274 CTGCAGATCCGGGGAGACCGAGCTGGCTGCGCTACTGCGAGCTG
Db	589	TATGACCTCATGAGAATCTCTGCAACCTCATGAGATGACCTCTG	648	121 TTACAGATCCAGGAGAACTGAGCTGGCTGCGCTACTGCGAGCTG
Qy	811	GAATTCCTCTCCCTGGACCGGTTCTGCGAGTACTCGCCCTGAGT	930	311 GGCGTCTGCCCCACCATCTCTGAGCATGTCGGGAGCTGAGCTCCCTGAGCCCTAACAT
Db	649	CACTTCACTTCTGGCGGCGCTCTGCACCCCGTCACTGCG	708	180 1 ATGGTGGTTAACGCCACGATGCCCAACCTGGGCT
Qy	871	GGGGTGAAGACCGGTTATGAGCTAACCTCTGGCGAGTACTCGCC	930	241 GGCGTCTGCCCCACCATCTCTGAGCATGTCGGGCTACTGCGCTG
Db	709	GTCGTCAGAGAGATCATGAGCTCTGGCGAGTACACAGGAGCTGT	768	300 451 GACTCTGCTAACGAGGTAAACCCCACACGGGACACTCCAGGCT
Qy	931	ATGATAAGAGTGTGCCAGAGGCCACAGGCTCTCAAGGATTACACCTC	990	510 301 GATTCTGCTAACGAGGTAAACCCCACACGGGACACTCCAGGCT
Db	769	GGCCTTACATCTCCGGAGAGGGACACCCCGCCCTCTACAGGGTTATG	828	570 630 648 668 690 728 750
Qy	991	TTTGGGTTGGGATCTGCGACGGTGTGTTCTTACTATGAGCACTGAA	1050	691 AAAGGAACTTCCACATGAGGAATCTGCACTGAGCTGAGCTG
Db	829	TTTCTCGCTTGGATCTGCGACGGTGTGTTCTTACTATGAGCACTGAA	888	631 AGGGGACTCTGAGCTGAGCTGGCTGAGCTGGCTGAGCTGG
Qy	1051	GGCTGTGTAAGTCCAGATGTTACGGGAATCACCGTTGA 1092		631 AGGGGACTCTGAGCTGAGCTGGCTGAGCTGGCTGAGCTGG
Db	889	GGCTTAATGGCTCCCTTACCATCTGGAGGACCTTCTGA 930		631 AGGGGACTCTGAGCTGAGCTGGCTGAGCTGGCTGAGCTGG
RESULT 9				
AY413337	AY413337	Homo sapiens ucP2 gene, virtual transcript, partial sequence, genomic survey sequence.	930 bp	DNA
DEFINITION				LINEAR GSS 17-DEC-2003
ACCESSION	AY413337			
VERSION	AY413337.1			
KEYWORDS	GSS.			
SOURCE				
ORGANISM	Homo sapiens (human)			

normalized version of this library is also available (NIH ZGC 7). Library was constructed by Open Biosystems (Huntsville, AL).

	ORIGIN
Db	529 AAAGGGACCTCCATGTTCTCGTAATGCCATGTCACTGTGAGCTGACC 588
Qy	751 TAGACATCTTAAAGAGAACCTGCTGACTAACCTGTCACACTCCCTGC 810
Db	589 TATGACTCTAAGATGCTCCTGAAGCCACCATGATGAGCTCCCTG 648
Qy	811 CACTTGTCTGCTGCTTGAGGACCTCTCTGCAAGAGCTAACCTCCCTGC 870
Db	649 CACTTACTCTGCTGCTTGAGGACCTCTCTGCAAGAGCTAACCTCCCTGC 648
Qy	871 GTGGTGAAGACCGCTATATGAACTCACCTCCAGCACTCTACCTCTAGAC 708
Db	709 GTGGTCAAGACGAGATACTGAACTCTGCTGCAAGAGCTAACCTCCCTGC 768
Qy	931 ATGATAAGATGTTGGCCAGAGGCCACAGCTTCAAGGATTACACCTCC 990
Db	769 GGCCTTACCATGCTCAGAAGAGGAGGAGGCTTCAAGGTTCTGCCTCC 828
Qy	991 TTTCAGTGGTGGATCTGGACCTGTTGTTGTTGAACTTAAAGGTTCTGAC 1050
Db	829 TTTCAGTGGTGGATCTGGACCTGTTGTTGAACTTAAAGGTTCTGAC 888
Qy	1051 GGCCTGATGAAGTCCAGATGTTACCGGAAACCGTTCA 1092
Db	889 GCCTCATGGCTGGCACTTCCGAGAGCTCCCTGCA 930
RESULT 10	
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LOCUS	AGENCOURT 16224310 NIH_ZGC_10 Danio rerio cDNA clone IMAGE:7050599
DEFINITION	5' mRNA Sequence.
ACCESSION	CK024683
VERSION	CK024683.1 GI:38550607
KEYWORDS	EST
SOURCE	Danio rerio (zebrafish)
ORGANISM	Danio rerio
REFERENCE	Eukaryota; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygi; Neopterygi; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
AUTHORS	NIH-MGC http://mgc.ncbi.nih.gov/
TITLE	Unpublished (1999)
JOURNAL	Office of Cancer Genomics
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)
CONTACT	Daniela S. Gerhard, Ph.D.
OFFICE	National Cancer Institute / NIH
Bldg:	31 Rm10107 Bethesda, MD 20892
Email:	cgapbs-r@mail.nih.gov
Tissue procurement:	Len Zon, Harvard
CDNA Library Preparation:	Open Biosystems
CDNA Library Arrayed By:	The I.M.A.G.E. Consortium (LILN)
DNA Sequencing by:	Agencourt Bioscience Corporation
Clone distribution:	MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILN at: http://image.liln.gov
Plate:	LILM14821 row: 1 column: 21
High quality sequence stop:	915.
FEATURES	
Source	
1.	Location/Qualifiers
1. 1101	/organism="Danio rerio"
/mol_type="mRNA"	
/db_xref="taxon:7955"	
/clone="IMAGE:7050599"	
/tissue_type="whole body"	
/lab_host="DHIB"	
/clone_id="NIH_ZGC_10"	
/note="Vector": pExpress1; Site 1: NotI; Site 2: EcoRV;	
Bulk tissue was collected from a whole adult individual from the Tuebingen strain. 1st strand cDNA was primed with a Not I - oligo(dt) primer, double-stranded cDNA was cloned into the Not I and EcoRV sites of pExpress-1.	
library was size-selected for >1 kb fragments. A	

RESULT 11		Db	362	TCCCTTTTCTGGTCTGGGATCCTGATCTGGTGTGTCACCTAGAGATGAA	421
BM986146	BN986146	Qy	1048	CGGGCCCTGATGAAGTCAGATGTTACGGAAACCGTTGACAGAGAGAGSC	1107
LOCUS	BN986146	Db	422	CGGCCTTGATGAAGTCAGATGAGCTTCAAGACGAGCTTCATTGAGACG-----	476
DEFINITION	LM24-HW00113 Bos taurus LM-24-HW cDNA library Bos taurus cDNA clone	Qy	1108	CACTGGTACTAAGCTGTGCGAAGACAGTTAAGATGGAGAACGTCACCCA	1167
VERSION	BN986146.1	Db	477	-GCTACTGTTAGTAGACAAACAGTTAAGGTGGATAAGCAGTGGTCATC	534
KEYWORDS	EST.	Qy	1168	CACATGGACACAGGCCACAGTTTACAGA-ACTGTGTTACTTGCTGATTA	1226
SOURCE	Bos taurus (cow)	Db	535	CACAGGACACAGCCACATGTGTTACAGAAGCTGTTACTTGCTGACTCA	594
ORGANISM	Bos taurus	Qy	1227	GAAC 1231	
REFERENCE	Bikaroya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.	Db	595	GAGAC 599	
AUTHORS	I. (bases 1 to 673)	Qy			
JOURNAL	Yoon, D.H., Jang, Y.S., Kim, T.H., Park, B.W., Lee, H.K., Chung, E.R., Sun, S.S. and Cheong, I.C.	Db			
TITLE	Gene Expression Profiling of the Bovine skeletal muscle	Qy			
COMMENT	Unpublished (2002)	Db			
Contact:	Dr. Du-Rak Yoon	Qy			
National Livestock Research Institute, RDA	564 Omochun-dong, Suwon, 441-350, Korea	Db			
Tel:	82 31 290 1593	Qy			
Fax:	82 31 290 1592	Db			
Insert Length:	821 Std Error: 0.00	Qy			
Seq primer:	CAAGGACAGGTATGAC	Db			
POLYA>No.		Qy			
FEATURES	Location/Qualifiers	Db			
source	1. . 673 /organism="Bos taurus"	Qy			
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	/db_xref="taxon:9913"	Qy			
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	/sex="Six males mixed"	Qy			
	/tissue="Longissimus dorsi"	Db			
	/tissue_type="myocyte"	Qy			
	/day_stage="4 months old"	Db			
	/cell_type="XLI-BlueMR strain"	Qy			
	/lab_host="XLI-BlueMR strain"	Db			
	/clone lib="Bos taurus LM-24-HW cDNA library"	Qy			
	/notes="Organ: skeletal muscle; Vector: Uni-ZAPXR; site_1: ECORI; site_2: Xba I"	Db			
ORIGIN		Qy			
Query Match	35.3%; Score 434.2; DB 12; Length 673;	Db			
Best Local Similarity	95.8%; Pred. No. 1.2e-86;	Qy			
Matches	519; Conservative 0; Mismatches 78; Indels 8; Gaps 3;	Db			
FEATURES	Location/Qualifiers	Qy			
source	1. . 612 /organism="Homo sapiens"	Db			
	/mol_type="mRNA"	Qy			
	/db_xref="taxon:9606"	Db			
	/clone="IMAGE:4291158"	Qy			
	/lab_host="DH10B (T1 Phage-resistant)"	Db			
	/clone.lib="NIH_MGC_61"	Qy			
	/note="Organ: muscle (skeletal); Vector: PDNR-LIB	Db			
	(Clontech); Site 1: SFI1 (ggccgcctcgcc); Site 2: SFI1 (ggccattatggcc); 5' and 3' adaptors were used in cloning, as follows: 5' adaptor sequence: 5'-CACGGCCATATGCC-3', and 3' adaptor sequence: 5'-ATTCAGACGCCAGGCCGACATG-BP(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 1.0-4.0 kb). 1,115 colonies contained inserts by PCR. This library was enriched for full-length clones and web constructed by Clontech Laboratories (Palo Alto, CA)."	Qy			
ORIGIN		Qy			
Query Match	35.2%; Score 432.8; DB 10; Length 612;	Db			
Best Local Similarity	98.6%; Pred. No. 2.4e-86;	Qy			
Matches	489; Conservative 0; Mismatches 2; Indels 5; Gaps 5;	Db			
FEATURES	Location/Qualifiers	Qy			
source	1. . 612 /organism="Homo sapiens"	Db			
	/mol_type="mRNA"	Qy			
	/db_xref="taxon:9606"	Db			
	/clone="IMAGE:4291158"	Qy			
	/lab_host="DH10B (T1 Phage-resistant)"	Db			
	/clone.lib="NIH_MGC_61"	Qy			
	/note="Organ: muscle (skeletal); Vector: PDNR-LIB	Db			
	(Clontech); Site 1: SFI1 (ggccgcctcgcc); Site 2: SFI1 (ggccattatggcc); 5' and 3' adaptors were used in cloning, as follows: 5' adaptor sequence: 5'-CACGGCCATATGCC-3', and 3' adaptor sequence: 5'-ATTCAGACGCCAGGCCGACATG-BP(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 1.0-4.0 kb). 1,115 colonies contained inserts by PCR. This library was enriched for full-length clones and web constructed by Clontech Laboratories (Palo Alto, CA)."	Qy			
ORIGIN		Qy			
Query Match	35.2%; Score 432.8; DB 10; Length 612;	Db			
Best Local Similarity	98.6%; Pred. No. 2.4e-86;	Qy			
Matches	489; Conservative 0; Mismatches 2; Indels 5; Gaps 5;	Db			
FEATURES	Location/Qualifiers	Qy			
source	1. . 612 /organism="Homo sapiens"	Db			
	/mol_type="mRNA"	Qy			
	/db_xref="taxon:9606"	Db			
	/clone="IMAGE:4291158"	Qy			
	/lab_host="DH10B (T1 Phage-resistant)"	Db			
	/clone.lib="NIH_MGC_61"	Qy			
	/note="Organ: muscle (skeletal); Vector: PDNR-LIB	Db			
	(Clontech); Site 1: SFI1 (ggccgcctcgcc); Site 2: SFI1 (ggccattatggcc); 5' and 3' adaptors were used in cloning, as follows: 5' adaptor sequence: 5'-CACGGCCATATGCC-3', and 3' adaptor sequence: 5'-ATTCAGACGCCAGGCCGACATG-BP(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 1.0-4.0 kb). 1,115 colonies contained inserts by PCR. This library was enriched for full-length clones and web constructed by Clontech Laboratories (Palo Alto, CA)."	Qy			
ORIGIN		Qy			
Query Match	35.2%; Score 432.8; DB 10; Length 612;	Db			
Best Local Similarity	98.6%; Pred. No. 2.4e-86;	Qy			
Matches	489; Conservative 0; Mismatches 2; Indels 5; Gaps 5;	Db			
FEATURES	Location/Qualifiers	Qy			
source	1. . 612 /organism="Homo sapiens"	Db			
	/mol_type="mRNA"	Qy			
	/db_xref="taxon:9606"	Db			
	/clone="IMAGE:4291158"	Qy			
	/lab_host="DH10B (T1 Phage-resistant)"	Db			
	/clone.lib="NIH_MGC_61"	Qy			
	/note="Organ: muscle (skeletal); Vector: PDNR-LIB	Db			
	(Clontech); Site 1: SFI1 (ggccgcctcgcc); Site 2: SFI1 (ggccattatggcc); 5' and 3' adaptors were used in cloning, as follows: 5' adaptor sequence: 5'-CACGGCCATATGCC-3', and 3' adaptor sequence: 5'-ATTCAGACGCCAGGCCGACATG-BP(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 1.0-4.0 kb). 1,115 colonies contained inserts by PCR. This library was enriched for full-length clones and web constructed by Clontech Laboratories (Palo Alto, CA)."	Qy			
ORIGIN		Qy			
Query Match	35.2%; Score 432.8; DB 10; Length 612;	Db			
Best Local Similarity	98.6%; Pred. No. 2.4e-86;	Qy			
Matches	489; Conservative 0; Mismatches 2; Indels 5; Gaps 5;	Db			
FEATURES	Location/Qualifiers	Qy			
source	1. . 612 /organism="Homo sapiens"	Db			
	/mol_type="mRNA"	Qy			
	/db_xref="taxon:9606"	Db			
	/clone="IMAGE:4291158"	Qy			
	/lab_host="DH10B (T1 Phage-resistant)"	Db			
	/clone.lib="NIH_MGC_61"	Qy			
	/note="Organ: muscle (skeletal); Vector: PDNR-LIB	Db			
	(Clontech); Site 1: SFI1 (ggccgcctcgcc); Site 2: SFI1 (ggccattatggcc); 5' and 3' adaptors were used in cloning, as follows: 5' adaptor sequence: 5'-CACGGCCATATGCC-3', and 3' adaptor sequence: 5'-ATTCAGACGCCAGGCCGACATG-BP(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 1.0-4.0 kb). 1,115 colonies contained inserts by PCR. This library was enriched for full-length clones and web constructed by Clontech Laboratories (Palo Alto, CA)."	Qy			
ORIGIN		Qy			
Query Match	35.2%; Score 432.8; DB 10; Length 612;	Db			
Best Local Similarity	98.6%; Pred. No. 2.4e-86;	Qy			
Matches	489; Conservative 0; Mismatches 2; Indels 5; Gaps 5;	Db			
FEATURES	Location/Qualifiers	Qy			
source	1. . 612 /organism="Homo sapiens"	Db			
	/mol_type="mRNA"	Qy			
	/db_xref="taxon:9606"	Db			
	/clone="IMAGE:4291158"	Qy			
	/lab_host="DH10B (T1 Phage-resistant)"	Db			
	/clone.lib="NIH_MGC_61"	Qy			
	/note="Organ: muscle (skeletal); Vector: PDNR-LIB	Db			
	(Clontech); Site 1: SFI1 (ggccgcctcgcc); Site 2: SFI1 (ggccattatggcc); 5' and 3' adaptors were used in cloning, as follows: 5' adaptor sequence: 5'-CACGGCCATATGCC-3', and 3' adaptor sequence: 5'-ATTCAGACGCCAGGCCGACATG-BP(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 1.0-4.0 kb). 1,115 colonies contained inserts by PCR. This library was enriched for full-length clones and web constructed by Clontech Laboratories (Palo Alto, CA)."	Qy			
ORIGIN		Qy			
Query Match	35.2%; Score 432.8; DB 10; Length 612;	Db			
Best Local Similarity	98.6%; Pred. No. 2.4e-86;	Qy			
Matches	489; Conservative 0; Mismatches 2; Indels 5; Gaps 5;	Db			
FEATURES	Location/Qualifiers	Qy			
source	1. . 612 /organism="Homo sapiens"	Db			
	/mol_type="mRNA"	Qy			
	/db_xref="taxon:9606"	Db			
	/clone="IMAGE:4291158"	Qy			
	/lab_host="DH10B (T1 Phage-resistant)"	Db			
	/clone.lib="NIH_MGC_61"	Qy			
	/note="Organ: muscle (skeletal); Vector: PDNR-LIB	Db			
	(Clontech); Site 1: SFI1 (ggccgcctcgcc); Site 2: SFI1 (ggccattatggcc); 5' and 3' adaptors were used in cloning, as follows: 5' adaptor sequence: 5'-CACGGCCATATGCC-3', and 3' adaptor sequence: 5'-ATTCAGACGCCAGGCCGACATG-BP(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 1.0-4.0 kb). 1,115 colonies contained inserts by PCR. This library was enriched for full-length clones and web constructed by Clontech Laboratories (Palo Alto, CA)."	Qy			
ORIGIN		Qy			
Query Match	35.2%; Score 432.8; DB 10; Length 612;	Db			
Best Local Similarity	98.6%; Pred. No. 2.4e-86;	Qy			
Matches	489; Conservative 0; Mismatches 2; Indels 5; Gaps 5;	Db			
FEATURES	Location/Qualifiers	Qy			
source	1. . 612 /organism="Homo sapiens"	Db			
	/mol_type="mRNA"	Qy			
	/db_xref="taxon:9606"	Db			
	/clone="IMAGE:4291158"	Qy			
	/lab_host="DH10B (T1 Phage-resistant)"	Db			
	/clone.lib="NIH_MGC_61"	Qy			
	/note="Organ: muscle (skeletal); Vector: PDNR-LIB	Db			
	(Clontech); Site 1: SFI1 (ggccgcctcgcc); Site 2: SFI1 (ggccattatggcc); 5' and 3' adaptors were used in cloning, as follows: 5' adaptor sequence: 5'-CACGGCCATATGCC-3', and 3' adaptor sequence: 5'-ATTCAGACGCCAGGCCGACATG-BP(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 1.0-4.0 kb). 1,115 colonies contained inserts by PCR. This library was enriched for full-length clones and web constructed by Clontech Laboratories (Palo Alto, CA)."	Qy			
ORIGIN		Qy			
Query Match	35.2%; Score 432.8; DB 10; Length 612;	Db			
Best Local Similarity	98.6%; Pred. No. 2.4e-86;	Qy			
Matches	489; Conservative 0; Mismatches 2; Indels 5; Gaps 5;	Db			
FEATURES	Location/Qualifiers	Qy			
source	1. . 612 /organism="Homo sapiens"	Db			
	/mol_type="mRNA"	Qy			
	/db_xref="taxon:9606"	Db			
	/clone="IMAGE:4291158"	Qy			
	/lab_host="DH10B (T1 Phage-resistant)"	Db			
	/clone.lib="NIH_MGC_61"	Qy			
	/note="Organ: muscle (skeletal); Vector: PDNR-LIB	Db			
	(Clontech); Site 1: SFI1 (ggccgcctcgcc); Site 2: SFI1 (ggccattatggcc); 5' and 3' adaptors were used in cloning, as follows: 5' adaptor sequence: 5'-CACGGCCATATGCC-3', and 3' adaptor sequence: 5'-ATTCAGACGCCAGGCCGACATG-BP(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 1.0-4.0 kb). 1,115 colonies contained inserts by PCR. This library was enriched for full-length clones and web constructed by Clontech Laboratories (Palo Alto, CA)."	Qy			
ORIGIN		Qy			
Query Match	35.2%; Score 432.8; DB 10; Length 612;	Db			
Best Local Similarity	98.6%; Pred. No. 2.4e-86;	Qy			
Matches	489; Conservative 0; Mismatches 2; Indels 5; Gaps 5;	Db			
FEATURES	Location/Qualifiers	Qy			
source	1. . 612 /organism="Homo sapiens"	Db			
	/mol_type="mRNA"	Qy			
	/db_xref="taxon:9606"	Db			
	/clone="IMAGE:4291158"	Qy			
	/lab_host="DH10B (T1 Phage-resistant)"	Db			
	/clone.lib="NIH_MGC_61"	Qy			
	/note="Organ: muscle (skeletal); Vector: PDNR-LIB	Db			
	(Clontech); Site 1: SFI1 (ggccgcctcgcc); Site 2: SFI1 (ggccattatggcc); 5' and 3' adaptors were used in cloning, as follows: 5' adaptor sequence: 5'-CACGGCCATATGCC-3', and 3' adaptor sequence: 5'-ATTCAGACGCCAGGCCGACATG-BP(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 1.0-4.0 kb). 1,115 colonies contained inserts by PCR. This library was enriched for full-length clones and web constructed by Clontech Laboratories (Palo Alto, CA)."	Qy			
ORIGIN		Qy			
Query Match	35.2%; Score 432.8; DB 10; Length 612;	Db			
Best Local Similarity	98.6%; Pred. No. 2.4e-86;	Qy			
Matches	489; Conservative 0; Mismatches 2; Indels 5; Gaps 5;	Db			
FEATURES	Location/Qualifiers	Qy			
source	1. . 612 /organism="Homo sapiens"	Db			
	/mol_type="mRNA"	Qy			
	/db_xref="taxon:9606"	Db			
	/clone="IMAGE:4291158"	Qy			
	/lab_host="DH10B (T1 Phage-resistant)"	Db			
	/clone.lib="NIH_MGC_61"	Qy			
	/note="Organ: muscle (skeletal); Vector: PDNR-LIB	Db			
	(Clontech); Site 1: SFI1 (ggccgcctcgcc); Site 2: SFI1 (ggccattatggcc); 5' and 3' adaptors were used in cloning, as follows: 5' adaptor sequence: 5'-CACGGCCATATGCC-3', and 3' adaptor sequence: 5'-ATTCAGACGCCAGGCCGACATG-BP(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 1.0-4.0 kb). 1,115 colonies contained inserts by PCR. This library was enriched for full-length clones and web constructed by Clontech Laboratories (Palo Alto, CA)."	Qy			
ORIGIN		Qy			
Query Match	35.2%; Score 432.8; DB 10; Length 612;	Db			
Best Local Similarity	98.6%; Pred. No. 2.4e-86;	Qy			
Matches	489; Conservative 0; Mismatches 2; Indels 5; Gaps 5;	Db			
FEATURES	Location/Qualifiers	Qy			
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	/mol_type="mRNA"	Qy			
	/db_xref="taxon:9606"	Db			
	/clone="IMAGE:4291158"	Qy			
	/lab_host="DH10B (T1 Phage-resistant)"	Db			
	/clone.lib="NIH_MGC_61"	Qy			
	/note="Organ: muscle (skeletal); Vector: PDNR-LIB	Db			
	(Clontech); Site 1: SFI1 (ggccgcctcgcc); Site 2: SFI1 (ggccattatggcc); 5' and 3' adaptors were used in cloning, as follows: 5' adaptor sequence: 5'-CACGGCCATATGCC-3', and 3' adaptor sequence: 5'-ATTCAGACGCCAGGCCGACATG-BP(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 1.0-4.0 kb). 1,115 colonies contained inserts by PCR. This library was enriched for full-length clones and web constructed by Clontech Laboratories (Palo Alto, CA)."	Qy			
ORIGIN		Qy			
Query Match	35.2%; Score 432.8; DB 10; Length 612;	Db			
Best Local Similarity	98.6%; Pred. No. 2.4e-86;	Qy			

/issue\_type="whole body"  
 /lab\_host="DH10B"  
 /clone.Lib=NIH ZGC\_10"  
 /note="vector: pXpress1; site\_1: NotI; site\_2: EcoRV;  
 Bulk tissue was collected from a whole adult individual  
 from the Tübingen strain. 1st strand cDNA was primed with  
 a Not I - oligo(dT) cloned into the Not I and EcoRV sites of pXpress-1.  
 library was size-selected for >1 kb fragments. A  
 normalized version of this library is also available  
 (NIH\_ZGC\_7). Library was constructed by Open Biosystems  
 (Huntsville, AL)."

	ORIGIN
Query	Match Similarity 34.4%; Score 423; DB 14; Length 1181;
Query	Best Local Similarity 69.6%; Pred. No. 5.2e-84; Matches 605; Conservative 0; Mismatches 255; Indels 9; Gap 2;
Db	Matches 605; Conservative 0; Mismatches 255; Indels 9; Gap 2;
Query	191 TGGCGTGAACTTCCTGGGGCAGCCACGCTTACCTTC 250
Db	6 TGACTGTGAAGGTGTAGACGAGACGCCGCTGATGCTCACCTTC 65
Db	349 GTCCAGAGGCCCGCTGTGCACTGGCCATCTGACATGG 408
Query	361 CGGAGTCAGGTTCCCTGAGCCCTAACATGGCTGTGGGGCTGAGGCGATG 420
Db	409 CGGAGTCAGGTTCCCTGAGCCCTAACATGGCTGTGGGGCTGAGGCGATG 467
Query	421 ACTCTCCATCCATGCCCTATGCTCTCAAGCAGTGTACCCCA- 479
Db	468 AGCTTGGCTCATCGCCATGGCTCTACGACTCGTCAAGCAGGTACACCCCA 527
Query	480 AGGGCGGACACTCC 495
Db	528 AGGGCGGACACTC 543
RESULT 13	
CK025514	CK025514 1181 bp mRNA Linear EST 26-NOV-2003
LOCUS	1181 bp mRNA
DEFINITION	Danio rerio cDNA clone IMAGE:7050849
ACCESSION	5', mRNA sequence.
VERSION	CK025514
KEYWORDS	GI:38551438
SOURCE	Danio rerio (zebrafish)
ORGANISM	Danio rerio
Bukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.	
REFERENCE	1 (bases 1 to 1181)
AUTHORS	NTH-MGC http://mgc.ncbi.nih.gov/
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics	National Cancer Institute / NIH
Bldg. 31 Rm10107 Bethesda, MD 20892	Email: cgabs@MAIL.NIH.GOV
Tissue Procurement: Len Zon, Harvard	CDNA Library Preparation: Open Biosystems
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)	DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at:	http://image.ILNL.gov
Plate: ILNM14222 row: g column: 07	High quality sequence step: 842.
FEATURES	Location/Qualifiers
source	1. .1181 /organism="Danio rerio" /mol_type="mRNA" /db_xref="taxon:7955" /clone="IMAGE:7050849"



/mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="NMAGE\_5148915"  
 /tissue\_type="tumor, gross tissue"  
 /dev\_stage="7 months"  
 /lab\_host="DH10B"  
 /clone.lib="NCI\_CGP\_Man5"  
 /note="Organ: mammary; Vector: pCMW-SPORT6; Site\_1: Sali;  
 Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
 Library constructed by Life Technologies. Investigators  
 providing samples: Lothar Hennighausen/Robin Humphreys,  
 NIH"

## ORIGIN

Query Match Similarity 32.9%; Score 405.4; DB 12; Length 927;  
 Best Local Similarity 71.8%; Pred. No. 4.1e-80; Mismatches 0; Indels 17; Gaps 5;  
 Matches 605; Conservative 0; Mismatches 221; Indels 17; Gaps 5;

Qy 214 GGCACAGCAGCTGTTGCTGACTCGTACTTCACAGCAACAGCCAGGTCGGC 273  
 Db 7 GTCGCACTGCTGCATGCAATCTCATCACTTCTCTCTGATACGCCAAGGTCGG 66

Qy 274 CTGCAAGATCCAGGGGAGAACAGGGC--GTCAGAGGGCGGTGTGAGTAGCT 330  
 Db 67 CTGCAAGATCCAGGGGAGAACAGGGC--GTCAGAGGGCGGTGTGAGTAGCT 126

Qy 331 GCGGTGCTGGGACCATCTGACCATGTCGGAATGTCGACTGAGGGTCCAGGCG 390  
 Db 127 GCGGTGCTGGGACCATCTGACCATGTCGCACTGAGGGTCCAGGCG 186

Qy 391 GCGCTGCTGGGCGCTCGAGGCGATGACTTCCTCATCCCATCGGCTCTAT 450  
 Db 187 GCGCTGCTGGGCGCTCGAGGCGATGACTTCCTCATCGGCTCTAT 246

Qy 451 GCTCCGTCAGGAGGTGACACCCCCAAAGGGGGAAACTCCAGCTACTACCG 510  
 Db 247 GACTCTCTCAACAGTTCTACACACAGGTTCTACACACAGGTTCTACACAGG 303

Qy 511 ATTTTGCGCGGTGACACAGGAGGCTGACCTGTCGCTCCAGGCCACAGATGTG 570  
 Db 304 CTCCTGGCAGGTAGCACCAACAGTGCCCTGGCGTGTACGCCAGCTACAGATGTG 363

Qy 571 GTGAAAGTCCGATTCTAGGCCAGCATACCTCGGGCATCAAGGAGGAGGAAATAC 630  
 Db 364 GTAAAGGPPCCGCTTCCAGGC-----TCAGGCCCGCTGTGTGGAGATAAC 414

Qy 631 ACGGGGACTATGACGCCATCGAGAACCTCGCAGGGAGGAGTCAGGGCTGTG 690  
 Db 415 CGAGACTCTGTTGAAAGCTACAGAACATTGACAGAGAGGGATCCGGCGCTGTG 474

Qy 691 AAAGGAACCTTCCCAAATCTGAGGATGTGTATCGTCACCTGTGCTGAGGGGTGA-C 749  
 Db 475 AAGGGACTCTCCCAAATGTCGCCGTTATGTCATGTCACCTGTGCTGAGGGTGA-C 534

Qy 750 CTAGGAGATCTCAAGGAGAGCTGCTGACTAACACCTGCTCACTGACAACTCCCTG 809  
 Db 535 CTATGACTCTCAACAGTACTCTCTCTGAAACCAACTCTCATACAGATGACTCTCCCTG 594

Qy 810 CACTTGCTCTGCTGCTTGGACCCGGCTCTGCTGCCACAGTGTGCTCCGGTGA 869  
 Db 595 CCACTTCACTCTGCTGCTTGGACCCGGCTCTGCTGCCACAGTGTGCTCCGGTGA 654

Qy 870 CCGGGTGAAGACCCGGTATATGACTCACCTCAGGGCAGTCTGAGGGTCAATGCTTC 929  
 Db 655 TCTGGTCAAGAGAGATACATGACTCTGCTTGGCGTGAACCTGAGGGTCACTG 714

Qy 930 TTGTGATAAGAGATGCTGCGACGGTGTGTTGTTGTAACCTATGAGACTGAGAC 989  
 Db 715 TCCCTTACATCTCCGGACAGGGGACCCGGCGCTCTCAAGGGTCAATGCTTC 774

Qy 990 CTTTGGTGGTGGGATCTGGACAGCTGTTGTTGTTGTAACCTATGAGACTGAGAC 1049

Db 775 CTTTCHCCGCTTGGGATCTGG-ACCTAGTGAATGTTGACCTATGAGCAAGTCAAAAGA 833  
 Qy 1050 GGC 1052  
 Db 834 GCC 836

Search completed: May 18, 2004, 14:45:31  
 Job time : 3081 BECS

Run on: May 18, 2004, 06:43:51 ; Search time 525 Seconds  
           (without alignments)  
           9961.013 Million cell updates/sec

Title: US-09-422-410-3  
       Perfect score:  
       1 ttcctggatggaggccctagg.....ttgttgctgattcaagaac 1231  
       Score:  
       IDENTITY\_NUC  
       Gapov 10.0 , Gapext 1.0

Scoring table: Gapext 1.0

Searched: 337863 seqs, 2124699041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
       Maximum DB seq length: 2000000000

post-processing: Minimum Match 0%  
       Maximum Match 100%  
       Listing first 45 summaries

SUMMARIES			
Result No.	Score	Query Length	DB ID
1	1231	100.0	AAV72690
2	1231	100.0	ABQ72999
3	1202.2	97.7	AAV84254
4	1185.2	96.3	AAV71710
5	1146.4	93.1	AAV46055
6	1146.4	93.1	ADD08530
7	1146.4	93.1	ADD0499
8	1144.8	93.0	AAZ29245
9	1144.8	93.0	AAV54602
10	1010.8	82.1	AAK08507
11	981.4	79.7	AAV72691
12	981.4	79.7	AAZ29324
13	981.4	79.7	AAK14820
14	981.4	79.7	AAK02389
15	981.4	79.7	AB073000
16	967.8	1033	AAV1711
17	939.3	76.3	AAZ19969
18	939.4	76.3	AAH18849
19	934.4	75.9	AFF4745
20	934.4	75.9	AFF4745
21	732	59.5	AAV84307
22	732	59.5	AAV71227
23	732	59.5	AAZ90318

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS			
Result No.	Score	Match Length	DB ID
1	1231	2	AAV72690
2	1231	6	ABQ72999
3	1231	2	AAV84254
4	1231	2	AAV71710
5	1231	3	AAV46055
6	1231	4	ADD08530
7	1231	6	ADD0499
8	1231	3	AAZ29245
9	1231	2	AAV54602
10	1231	2	AAK08507
11	981.4	1132	AAZ29324
12	981.4	1132	AAK14820
13	981.4	1132	AAK02389
14	981.4	1132	AB073000
15	981.4	1132	AAV1711
16	967.8	1033	AAV7111
17	939.3	76.3	AAZ19969
18	939.4	76.3	AAH18849
19	934.4	75.9	AFF4745
20	934.4	75.9	AFF4745
21	732	59.5	AAV84307
22	732	59.5	AAV71227
23	732	59.5	AAZ90318

R

RESULTS

ID AAV72690 standard; cDNA; 1231 BP.  
   XX  
   AC AAV72690;  
   XX  
   DT 22-FEB-1999 (first entry)  
   XX  
   DE Human uncoupling protein UCP3L encoding cDNA.  
   XX  
   KW Human; uncoupling protein; UCP3L; UCP3S; oxidative phosphorylation;  
   KW adenosine triphosphate; mitochondria; skeletal muscle; gene therapy;  
   KW thermogenesis; heart; obesity; cachexia; type II diabetes; hypertension;  
   KW insulin sensitivity; neuromuscular disease; ss.  
   XX  
   OS Homo sapiens.  
   XX  
   FH KEY Location/Qualifiers  
   FT CDS 154..1092  
   FT /\*tag= "UCP3L"  
   FT /product= "UCP3L"  
   XX  
   PN W09850542-A1.  
   XX  
   PD 12-NOV-1998.  
   XX  
   PF 05-MAY-1998; 98WO-EP002645.  
   XX  
   PR 07-MAY-1997; 97CH-0001072.  
   XX  
   PA (NOVS ) NOVARTIS AG.  
   PA (NOVS ) NOVARTIS-ERFINDUNGEN VNRW GBS MBH.  
   XX  
   PT Giacobino J, Muzzin P, Boss O,  
   XX  
   DR WPI; 1998-610382/51.  
   DR -PSDB; AAW83379.

PT New human skeletal muscle uncoupling proteins UCP3L and UCP3S - useful for controlling thermogenesis in human skeletal muscle and heart, e.g. for treating obesity and cachexia.

PT The present sequence encodes human uncoupling protein UCP3L. UCP3 uncouples oxidative phosphorylation and synthesis of adenosine

CC triphosphate in the mitochondria of skeletal muscle. The coding sequences for UCP3L and UCP3S are useful for gene therapy of dysfunctions of thermogenesis in human skeletal muscle and heart which result from a lack of UCP3 and which can induce disorders such as obesity or cachexia.

CC Antisense oligonucleotides to UCP3L and UCP3S can be used for correcting an excess of UCP3. Modification of endogenous UCP3 activity (using activators or inhibitors of UCP3) is used to induce bodyweight loss (loss of adipose mass and maintenance of the lean mass) in all types of obesity by promoting the dissipation of energy; for preventing an excessive weight regain following restrictive food diet or after ceasing a physical training programme; for preventing and treating type II diabetes by improving sensitivity to insulin; for preventing hypertension; for increasing muscle mass in states of cachexia; for treatment of insufficiencies or disturbances of cardiac rhythm due to a dysfunction of UCP3; and for the treatment of neuromuscular diseases due to a dysfunction of UCP3. The uncoupling proteins can also be used to raise antibodies, e.g., for diagnosis. Knowledge of the UCP3 genes allows generation of transgenic animals, e.g., for screening substances which modify UCP3 expression or activity or for investigating the biological role of UCP3.

XX Sequence 1231 BP; 271 A; 371 C; 345 G; 244 T; 0 U; 0 Other;

Query Match 100.0%; Score 1231; DB 2; Length 1231;  
Best Local Similarity 100.0%; Pred. No. 3.5e-295; Mismatches 0; Indels 0; Gaps 0;

Matches 1231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ

QY 1 TCTCTGGATGAGGCCCTTCTGGAGGCCCTTCTGGCTGCGGTGAGGACTCACAGCC 60  
Db 1 TCTCTGGATGAGGCCCTTCTGGAGGCCCTTCTGGCTGCGGTGAGGACTCACAGCC 60  
Qy 61 CCACCGTGACTGAACGCCCAAGGCTTGAGGACAGCTCTTCCTTGACTCTCTGG 120  
Db 61 CCACCGTGACTGAACGCCCAAGGCTTGAGGACAGCTCTTCCTTGACTCTCTGG 120  
Qy 121 CCTAAAGGACTGGGAGACCTCCGGATATGGTGACTGAGCCTCAGAGGTGAGGTG 180  
Db 121 CCTAAAGGACTGGGAGACCTCCGGATATGGTGACTGAGCCTCAGAGGTGAGGTG 180  
Qy 181 CCTCCACCATGCTGTAAGTCTGGGGAGCACAGGAGCTTGCTGACT 240  
Db 181 CCTCCACCATGCTGTAAGTCTGGGGAGCACAGGAGCTTGCTGACT 240  
Qy 241 GTTACCTTTCACTGGACACASCCAAGSTCCGCCTCGAGATCAGGGAGAACCCAGGG 300  
Db 241 GTTACCTTTCACTGGACACAGGCAAGGTCGCCTCGAGATCAGGGAGAACCCAGGG 300  
Qy 301 GTCAGAGGGCGGGCTGGCGTACCGTGCCTGCGACCCCTTGACCATGTC 360  
Db 301 GTCAGAGGGCGGGCTGGCGTACCGTGCCTGCGACCCCTTGACCATGTC 360  
Qy 361 CGGACTGAGGGTCCTGAGGCTACATAGGAGCTGGTGGCGCTGAGGGAGATG 420  
Db 361 CGGACTGAGGGTCCTGAGGCTACATAGGAGCTGGTGGCGCTGAGGGAGATG 420  
Qy 421 AGCTTGCTTCACTGGCTCTATGACTCCGTCAGACGGGTTACCCCCCAA 480  
Db 421 AGCTTGCTTCACTGGCTCTATGACTCCGTCAGACGGGTTACCCCCCAA 480  
Qy 481 GGCGGAGAACCTCAGCTTACCCGGATTGCGCGTGCACACAGGAGCTG 540  
Db 481 GGCGGAGAACCTCAGCTTACCCGGATTGCGCGTGCACACAGGAGCTG 540  
Qy 541 GCGGTGACCTGTGCCAGCCACAGATGGTGGAGGTCGATTCAGCCACATAC 600  
Db 541 GCGGTGACCTGTGCCAGCCACAGATGGTGGAGGTCGATTCAGCCACATAC 600  
Qy 601 CTCGGCCATCCAGGAGCAAGAAATAGCGGACTATGGAGGCTACAGACATC 660  
Db 601 CTCGGCCATCCAGGAGCAAGAAATAGCGGACTATGGAGGCTACAGACATC 660  
Qy 661 GCGGGAGGAGGAGTGGGAGGACTTGCCAACTCATGGAGGAT 720

Db 661 GCCAGGGAGGAGGAGTCAAGGGCTGTGAAAGGACTTGTGCCAACATCATGGAGAAT 720  
Qy 721 GCTATGTCACTGNGCTGAGGTTGAGGACTACAGACATCTCAAGGAGAGCTGTGAC 780  
Db 721 GCTATGTCACTGNGCTGAGGTTGAGGACTACAGACATCTCAAGGAGAGCTGTGAC 780  
Qy 781 TACCACTGCTCACTGACAACCTCCCTGCACTTGTGCTGAGCTTGGCCGCTTC 840  
Db 781 TACCACTGCTCACTGACAACCTCCCTGCACTTGTGCTGAGCTTGGCCGCTTC 840  
Qy 841 TGTGCCACAGTGGCTGCCCTCCGGTGGAGCTGGTGGAGAGACCGTATACTCCT 900  
Db 841 TGTGCCACAGTGGCTGCCCTCCGGTGGAGCTGGTGGAGAGACCGTATACTCCT 900  
Qy 901 CCAGGCCAGTACTTCAGCCCTGAGTGTGAGTAAAGTAGGTGGCTGCCAGGGCCC 960  
Db 901 CCAGGCCAGTACTTCAGCCCTGAGTGTGAGTAAAGTAGGTGGCTGCCAGGGCCC 960  
Qy 961 ACAGCCTCTACAAAGGATTACACCTCCCTTGTGAGTGGTGGAGACCGTGTG 1020  
Db 961 ACAGCCTCTACAAAGGATTACACCTCCCTTGTGAGTGGTGGAGACCGTGTG 1020  
Qy 1021 ATGTTGCTAACCTATGAGCAGCTGAAAGCCCTGTGAAAGTCAAGTGTAGGGAA 1080  
Db 1021 ATGTTGCTAACCTATGAGCAGCTGAAAGCCCTGTGAAAGTCAAGTGTAGGGAA 1080  
Qy 1081 TCACCTTTGACAGACAAGAAAGCCACTGTGCTGAGCTTGGTCCGAAACCAGTTAG 1140  
Db 1081 TCACCTTTGACAGACAAGAAAGCCACTGTGCTGAGCTTGGTCCGAAACCAGTTAG 1140  
Qy 1141 ATGGAAAACGGTCATCACGCCACATGGACACCCACATGTTTACGAA 1200  
Db 1141 ATGGAAAACGGTCATCACGCCACATGGACACCCACATGTTTACGAA 1200  
Qy 1201 CTGTTGTTACTGTGCTGTGATCAAGAAC 1231  
Db 1201 CTGTTGTTACTGTGCTGTGATCAAGAAC 1231

RESULT 2  
ABQ7299  
ABQ7299 standard; cDNA; 1231 BP.  
XX  
AC  
ID ABQ7299;  
XX  
DT 20-SEP-2002 (first entry)  
XX  
DB UCP3L cDNA clone nucleotide sequence.

XX UCP3L; UCP3S; diabetes; obesity; diabetic related condition; GRP; gene therapy; antidiabetic; anorectic; cardiotropic; GI; anti-lipaemic; blood glucose; glucokinase regulatory protein; liver; hepatic triglyceride accumulation; fibringen; HDL; glucokinase; hepatic fatty acid oxidation; high density lipoprotein; glucose; gestational diabetes; hyperglycaemic related disorder; kidney; kidney related disorder; cardiovascular disorder; gene; BB.  
XX Unidentified.

XX  
PH Key Location/Qualifiers  
PT CDS 154..1092  
PT /\*tag= a  
PT /product= "UCP3L protein"  
XX  
PN US2002065239-A1.  
XX  
PP 30-MAY-2002.  
XX  
PP 14-MAR-2001; 2001US-00808457.  
XX  
PR 15-MAR-2000; 2000US-0266328P.  
XX  
(CPL/ CAPLAN S L.

	RESULT 3
AAV84254	
ID	AAV84254 standard; cDNA; 2340 BP.
XX	
AC	AAV84254;
XX	
DT	12-APR-1999 (first entry)
XX	
DE	Human uncoupling protein 3 (UCP3) cDNA
XX	
KW	Uncoupling protein 3; UCP3; human; obesity; gene therapy; db; XX
OS	Hypermetabolism; Homo sapiens.
XX	
FH	
Key	Location/Qualifiers

QY	1021	ATGTTCTAACCTATGGACGCTGAAACGGCCCTGTAAGTCCAGATTTACCGAA	1080
Db	1021	ATGTTCTAACCTATGGACGCTGAAACGGCCCTGTAAGTCCAGATTTACCGAA	1080
QY	1081	TGACCGTTGACAGAACAGAACGCCCCACTGGTAGCTAACGGTGTCCGAACCGATTAG	1140
Db	1081	TGACCGTTGACAGAACAGAACGCCCCACTGGTAGCTAACGGTGTCCGAACCGATTAG	1140
QY	1141	AATGGAGAACGGGCAATCCAGCACATGGACACAGAACGCCACAGTGTACAGAA	1200
Db	1141	AATGGAGAACGGGCAATCCAGCACATGGACACAGAACGCCACAGTGTACAGAA	1200
QY	1201	CCTGTTTACGTGTCTGATTGAGAAC	1231
Db	1201	CCTGTTTACGTGTCTGATTGAGAAC	1231



KW Uncoupling protein 3; UCP3; thermogenesis; mammal; enhancer; drug;  
 KW protein catabolism; anti-obesity; inhibitor; muscle wasting; infection;  
 KW HIV; cancer; tumour cachexia; muscle disease; muscular dystrophy;  
 KW non-insulin dependent diabetes mellitus; diagnosis; human; ds.  
 OS Homo sapiens.

XX

FH Location/Qualifiers

FT 1. .1220

FT /\*tag= b

FT /note= "reading frame 1; contains internal stop codons  
 which are not indicated in the corresponding protein  
 (AAW81588)"

FT 2. .1220

FT /\*tag= C

FT /note= "reading frame 2; contains internal stop codons  
 which are not indicated in the corresponding protein  
 (AAW81589)"

FT 3. .1220

FT /\*tag= d

FT /note= "reading frame 3; contains internal stop codons  
 which are not indicated in the corresponding protein  
 (AAW81590)"

FT 184. .1122

FT /\*tag= a

FT /product= "human UCP3"

XX W09845438-A1.

XX PD 15-OCT-1998.

XX PR 09-APR-1998; 98WO-US006959.

XX PR 12-MAY-1997; 97US-0046254P.

XX PR 15-JUL-1997; 97US-0089745.

XX PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CTRN.

XX PI Lowell BB, Flier JS;

XX DR WPI; 1998-594493/50, AAW81587, AAW81588, AAW81589, AAW81590.

XX PT New isolated uncoupling protein, UCP-3 - used to develop products for  
 modulating thermogenesis in tissues, e.g. for treating obesity or muscle  
 wasting caused by infection or cancer.

XX PS Claim 3; Fig 1A-C; 98pp; English.

XX CC This DNA encodes a human uncoupling protein 3 (ucp3). A host cell  
 transformed with a construct comprising the UCP3 nucleic acid can be used  
 for the recombinant production of the protein. The UCP3 is involved in  
 the regulation of thermogenesis in mammals. The nucleic acids (AAV1710  
 to AAV1717) can be used for identifying compounds which alter UCP3  
 activity. Enhancers of UCP3 can be used for enhancing protein catabolism  
 in a mammal and can be used as anti-obesity drugs. Inhibitors of UCP3 can  
 be used for inhibiting protein catabolism in a mammal such as inhibiting  
 muscle wasting. They can be used for curtailing muscle wasting due to  
 infection (e.g. HIV), cancer, tumour cachexia, muscle diseases (e.g.  
 muscular dystrophy) or as a possible treatment for non-insulin dependent  
 diabetes mellitus. The products can also be used for detection and  
 diagnosis

XX sequence 1220 BP; 267 A; 376 C; 345 G; 232 T; 0 U; 0 Other;

Query Match 96.3%; Score 1185.2; DB 2; Length 1220;  
 Best Local Similarity 99.7%; Pred. No. 7.9e-284;  
 Matches 1187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Ov 1 TCTGGGATGGGCCCTTGGAGCCCTTGTCGCGCCCTGTGGTGGAGGACTCACAGGCC 60

Ov 31 TCTGGGATGGGCCCTTGGAGCCCTTGTCGCGCCCTGTGGTGGAGGACTCACAGGCC 90

Qy 61 CCACCGCTGACTGAAGCCAGGCTGTCAGGACCTCTCTCTCTCTCTCTCTCTCG 120

Db 91 CCACCGCTGACTGAAGCCAGGCTGTCAGGACCTCTCTCTCTCTCTCTCG 150

Qy 121 CCTTAAGGACTGGAGGACCTTCAGGACTATGGTGAAGCTGAAGCCTCAAGCTG 180

Db 151 CCCTAACGGACTGGCAAGGCCTTCAGGACTATGGTGAAGCTGAAGCCTCAAGCTG 210

CDS

Qy 181 CCTCCACCATGGCTGTGAAGTCCCTGGGAGGACAGGAGCTCTCTCTCTCG 240

Db 211 CCTCCACCATGGCTGTGAAGTCCCTGGGAGGACAGGAGCTCTCTCTCG 270

Qy 241 GTTACCTTCACTGACGCAAGGCCAGGTGGCTGGCAGAATCCAGGGAGACAGGG 300

Db 271 GTTACCTTCACTGACGCAAGGCCAGGTGGCTGGCAGAATCCAGGGAGACAGGG 330

Qy 301 GTCCGACGCCGCTGCACTGAGCTGGCAGGCTGAGCTGACCCTGACCTGGT 360

Db 331 GTCCGACGCCGCTGCACTGAGCTGGCAGGCTGAGCTGACCCTGACCTGGT 390

Qy 361 CGGACTGAGGAGGCTGAGGCCACATGGCTGTGGCCGGCTGAGGCCAGTG 420

Db 391 CGGACTGAGGAGGCTGAGGCCACATGGCTGTGGCCGGCTGAGGCCAGTG 450

Qy 421 AGCTTGCTCATCGCATGGCTCATATGACTCGTCAAGCAGGTGACCCCCAA 480

Db 451 AGCTTGCTCATCGCATGGCTCATATGACTCGTCAAGCAGGTGACCCCCAA 510

Qy 481 GCGCGGAGAACCTCCAGCTCACTACCGGATTTGGCGCGCTGCAACAGGGCT 540

Db 511 GCGCGGAGAACCTCCAGCTCACTACCGGATTTGGCGCGCTGCAACAGGGCT 570

Qy 541 GGGTAGCTGTGCCAGGCCACAGATGGTGAAGGCTGGATTGAGCTACAC 600

Db 571 GGGTAGCTGTGCCAGGCCACAGATGGTGAAGGCTGGATTGAGCTACAC 630

Qy 601 CTGGGACATCAGGAGGAGCTGGGGCTGTGGAAAGGACTATGGACCCATAC 660

Db 631 CTGGGACATCAGGAGGAGCTGGGGCTGTGGAAAGGACTATGGACCCATAC 690

Qy 661 GCGAGGAGGAGGAGCTGGGGCTGTGGAAAGGACTATGGACCCATAC 720

Db 691 GCGAGGAGGAGGAGCTGGGGCTGTGGAAAGGACTATGGACCCATAC 750

Qy 721 GCTATCCTACTGTGCTGAGGTGGTGAACCTAGACATCTCAAGGAGACTGCGAC 780

Db 751 GCTATCCTACTGTGCTGAGGTGGTGAACCTAGACATCTCAAGGAGACTGCGAC 810

Qy 781 TACCACTGCTACTGACCACTTCCCTGCCACTTGTCTCTGCCCTTGAGCCGACTC 840

Db 811 TACCACTGCTACTGACCACTTCCCTGCCACTTGTCTCTGCCCTTGAGCCGACTC 870

Qy 841 TGTGCCACAGTGTGCTCCCTCCGGAGGACCTGGTGAAGACCCGGTATGACTC 900

Db 871 TGTGCCACAGTGTGCTCCCTCCGGAGGACCTGGTGAAGACCCGGTATGACTC 930

Qy 901 CGAGGGAGTACTTCAGCCCTGACTGTATGATAAGGAGTGGCTGCCAGGCCCC 960

Db 931 CGAGGGAGTACTTCAGCCCTGACTGTATGATAAGGAGTGGCTGCCAGGCCCC 990

Qy 961 ACAGCCCTTCAAGGAGTTACACCCCTTGAGTGAAGTCCAGGACTGTGGT 1020

Db 991 ACAGCCCTTCAAGGAGTTACACCCCTTGAGTGAAGTCCAGGACTGTGGT 1050

Qy 1021 ATGTTCTTACCTATGAGCAGGGACCTGATGAAGTCCAGATGTTACGGAA 1080

Db 1051 ATGTTCTTACCTATGAGCAGGGACCTGATGAAGTCCAGATGTTACGGAA 1110

Qy 1081 TCACCGTTGACAGCAAGAAGGCCACTGTGACCTAAGCTGTGCGAACCTGAG 1140

Db 1111 TCACTGTTGACAGCAAGAAGGCCACTGTGACCTAAGCTGTGCGAACCTGAG 1170

OY 1141 AATGGAGAAAACGCTGCACTCACGCCACACTGGACACAGACCCACAT 1190  
Db 1171 ATGGAGAAACGGTGATCAGCACATGGACACAGACCCACAT 1220

RESULT 5  
ID AAZ66055 standard; cDNA; 1193 BP.  
XX  
AC AAZ66055;  
XX  
DT 25-APR-2000 (first entry)

DE cDNA encoding a human uncoupling protein designated HIFCW60.  
XX Human; HIFCW60; mitochondrial uncoupling protein family; muscle wasting;  
KW uncoupling protein; wound; tissue repair; inflammation; cachexia; ss.  
XX  
OS Homo sapiens.

XX  
FH Key Location/Qualifiers  
FT 199 .1137  
FT /\*tag= a /product= "uncoupling protein"  
PT  
PN WO20002577-A1.  
XX 20-JAN-2000.  
XX 02-DEC-1998; 98WO-EP007802.  
PR 09-JUL-1998; 98GB-00014926.  
XX (SMK ) SMITHKLINE BRECHAM PLC.  
XX Clapham JC, Beeley LJ, Godden RJ;  
XX DR WPI, 2000-14752/13.  
DR P-PSDB; AAY54600.  
XX  
PT Use of uncoupling protein, polynucleotide and compound activating it, in  
PT treating wounds, inflammation, tissue repair, muscle wasting, and  
PT cachexia.  
XX  
PS Claim 9; Page 21; 29pp; English.

The present sequence encodes a HIFCW60 polypeptide, which is a member of the mitochondrial uncoupling protein family. The HIFCW60 polynucleotide has homology with human uncoupling protein 2. The polynucleotide sequence was isolated from a cDNA library derived from human skeletal muscle cell mRNA, and mRNA from the cell lines rhabdosarcoma, caski, and SHSY5Y. The protein is useful in producing antibodies and in screening for antagonist and agonist. The polynucleotide is useful as a reagent for diagnosing and determining susceptibility to the disease by detecting the mutation in the HIFCW60 gene. The polynucleotide, protein, and antibodies against the HIFCW60 are useful in screening for the compounds that have an effect on the production of mRNA and polypeptides in the cell. These compounds are used to treat wounds, tissue repair, inflammation, muscle wasting or cachexia.

SQ Sequence 1193 BP; 252 A; 369 C; 344 G; 228 T; 0 U; 0 Other;  
Query Match 93.1%; Score 1146.4; DB 3; Length 1193;  
Best Local Similarity 99.9%; Pred. No. 3.3e-274;  
Matches 1147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TCTGGGATGACCCCTTGGAGGACCCCTGTGCTGCTGGAGACTCACAGCC 60  
Db 46 TCTGGGATGACCCCTTGGAGGACCCCTGTGCTGCTGGAGACTCACAGCC 105  
OY 61 CCACCGCTGACTGAACGCCAAGCTGCTGCTGGAGACTCACAGCC 120  
Db 106 CCACCGCTGACTGAACGCCAAGCTGCTGCTGGAGACTCACAGCC 165

OY 121 CCTTAAGGACTGGAGGCCTCCAGACTATGGTGACTGAAGCTTCAGACGTG 180  
Db 166 CCTTAAGGACTGGAGGCCTCCAGACTATGGTGACTGAAGCTTCAGACGTG 225

OY 181 CCTCCACCATGGCTGAGTTCTGGGGAGGCAAGCAGCCTTGTGACTC 240  
Db 226 CCTCCACCATGGCTGAGTTCTGGGGAGGCAAGCAGCCTTGTGACTC 285  
OY 241 GTTACCTTCACTTGACACGCCAGGAGCCTGGAGACTATGGTGACTGA 300  
Db 346 GTTACCTTCACTTGACACGCCAGGAGCCTGGAGACTATGGTGACTGA 345

OY 361 GGACTGAGGTCCCTGAGCCCTAACATTGGCTGGTGGCCGCTGAGGGAGATG 420  
Db 406 CGGATGAGGTCCTGAGCCCTAACATTGGCTGGTGGCCGCTGAGGGAGATG 465

OY 421 AGCTTGCTTCATCGCATGGCTCTTGTGAGCTTCTCGCTGAGGGAGATG 480  
Db 526 GGGGGAGGAGCACTCCGGCTACTCCGGATTTGGCGCGCTGAGGGAGATG 585

OY 541 GGGGAGCTGTGCCAGCCACAGATGGTGAAGTGGTGGAGGTCGATTCA 600  
Db 586 GGGGAGCTGTGCCAGCCACAGATGGTGAAGTGGTGGAGGTCGATTCA 645

OY 601 CTGGGACCATCCAGGAGCACAGATAAGGGAGCATGGAGCCCTAGAACATC 660  
Db 646 CTGGGACCATCCAGGAGCACAGATAAGGGAGCATGGAGCCCTAGAACATC 705

OY 661 GCCAAGGAGGAGGAGTCAAGGGCTGTGAAAGGACATTCGGCAACATCATGAAAT 720  
Db 706 GCCAAGGAGGAGGAGTCAAGGGCTGTGAAAGGACATTCGGCAACATCATGAAAT 765

OY 721 GCTATGTCGACTGTGCTGAGGTGGTACCTACAGATCTCAAGGAAGCTGGAC 780  
Db 766 GCTATGTCGACTGTGCTGAGGTGGTACCTACAGATCTCAAGGAAGCTGGAC 825

OY 781 TACCACTGTCGACTCAACTTCCCCTGCACTTGTGCTGCTGGCTTGGGCCGCTC 840  
Db 826 TACCACTGTCGACTCAACTTCCCCTGCACTTGTGCTGCTGGCTTGGGCCGCTC 885

OY 841 TGTGCCAGAGTGACCTCCGGAGACGTGGAGACCGGTTATAACCT 900  
Db 886 TGTGCCAGAGTGACCTCCGGAGACGTGGAGACCGGTTATAACCT 945

OY 901 CCAGGCCAGTCTCAGCCCTCTACTGTATGATAAGATGGTGGCCAGGAGCCCC 960  
Db 946 CCAGGCCAGTCTCAGCCCTCTACTGTATGATAAGATGGTGGCCAGGAGCCCC 1005

OY 961 ACAGCTCTCACAGGGATTACACCCCTTGGTTGGATGATAGATGGTGGCCAGGAGCCCC 1020  
Db 1006 AGACCTCTCACAGGGATTACACCCCTTGGTTGGATGATAGATGGTGGCCAGGAGCCCC 1065

OY 1021 ATGGTCTTAACTTATGAGCACTGAGGGCCCTATGAGTCGAGATGTTACGGAA 1080  
Db 1066 ATGGTCTTAACTTATGAGCACTGAGGGCCCTATGAGTCGAGATGTTACGGAA 1125

OY 1081 TCACCGTTGACAGACAAGAAGGCCACTGTGACTTAAGTGTGCGAAACCGTTAG 1140  
Db 1126 TCACCGTTGACAGACAAGAAGGCCACTGTGACTTAAGTGTGCGAAACCGTTAG 1185

OY 1141 AATGGAA 1148  
Db 1186 AATGGAA 1193

RESULT 6  
 ID AAD08530 standard; cDNA; 1193 BP.  
 XX  
 AC AAD08530;  
 XX  
 DT 04-SEP-2001 (first entry)  
 XX Human uncoupling protein-3 (UCP3) cDNA.  
 XX Human; UCP3; uncoupling protein-3; chromosome 11q13; gene therapy;  
 KW atherosclerosis; hypercholesterolaemia; antilipemic; sb.  
 XX Homo sapiens.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT 199 .1137 /\*tag= a  
 FT /product= "Human UCP3 protein"  
 FT  
 XX WO200143760-A2.  
 XX  
 PD 21-JUN-2001.  
 XX 18-DEC-2000; 2000WO-EP012931.  
 XX PR 17-DEC-1999; 99GB-00030100.  
 XX PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX PI Clapham JC;  
 XX DR WPI; 2001-398073/42.  
 DR P-PSDB; AAE04298.  
 XX PT Use of a compound selected from UCP3 polypeptide, a compound which  
 activates the polypeptide, or a polynucleotide encoding the polypeptide,  
 for treating atherosclerosis or hypercholesterolaemia.  
 XX PS Claim 9; Page 19; 24pp; English.  
 XX CC The present sequence is a cDNA encoding human UCP3 (uncoupling protein-3)  
 CC protein. UCP3 gene is located in chromosome 11q13. UCP3 protein and  
 CC polynucleotides encoding them are useful for identifying agonist  
 CC compounds which are potentially useful in therapy. UCP3 protein is useful  
 for inducing an immunological response, as immunogen to produce  
 CC antibodies immunospecific for UCP3 protein, and in a method for the  
 CC structure-based design of an agonist for UCP3 protein. UCP3 sequences are  
 CC useful to configure screening methods for detecting the effect of added  
 CC components on the production of mRNA and polypeptide in cells. UCP3 DNA  
 CC is used in gene therapy. A compound which activates UCP3 protein or a  
 CC polynucleotide encoding UCP3 protein are used for the manufacture of  
 CC medicament for treating atherosclerosis or hypercholesterolaemia  
 XX SQ Sequence 1193 BP; 252 A; 369 C; 344 G; 228 T; 0 U; 0 Other;  
 Query Match 93.1%; Score 1146.4; DB 4; Length 1193;  
 Best Local Similarity 99.9%; Pred. No. 3\_3e-274;  
 Matches 1147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 181 CCTCCCCACCATGGCTGTGAAAGTTCTGGGGCAGCACCCAGCTGTTTGCTGACCTC 240  
 Db 226 CCTCCACCATGGCTGTGAAAGTTCTGGGGCAGCACCCAGCTGTTTGCTGACCTC 285  
 Qy 241 GTTACCTTTCACTGACATGCCAGGCGCTGCACATGCCAGGCGCTGCAATCCAGGGAGAACCGGG 300  
 Db 286 GTTACCTTTCACTGACATGCCAGGCGCTGCAATCCAGGGAGAACCGGG 345  
 Qy 301 GTCCAGACGGGGGGCTGTCAGTACCTGGCTGGCTGCTGGCACCATCCCTGACCATGGTG 360  
 Db 346 GTCCAGACGGGGGGCTGTCAGTACCTGGCTGGCTGCTGGCACCATCCCTGACCATGGTG 405  
 Qy 361 CGGACTGAGGCTCCCTGAGCCCTTACAATGGCTGTGGCTGCTGGCTGAGGGAGAGTG 420  
 Db 406 CGGACTGAGGCTCCCTGAGCCCTTACAATGGCTGTGGCTGCTGGCTGAGGGAGAGTG 465  
 Qy 421 AGCTTGCTGCTCATGGCATGGCTCTATGACTCGGTAGCTGGCTGAGGGAGAGTG 480  
 Db 466 AGCTTGCTGCTCATGGCATGGCTCTATGACTCGGTAGCTGGCTGAGGGAGAGTG 525  
 Qy 481 GGGGGGAACTCCAGCTACTACGGATTGGCGCTGACCAACAGGGCCATG 540  
 Db 526 GGGGGGAACTCCAGCTACTACGGATTGGCGCTGACCAACAGGGCCATG 585  
 Qy 541 GCGGTGACTCTGGCCAGCCACAGATGTTGTAAGGCTTCAAGGCGAGTACAC 600  
 Db 586 AGGGTGACTCTGGCCAGCCACAGATGTTGTAAGGCTTCAAGGCGAGTACAC 645  
 Qy 601 CTGGGGCATCCAGGGAGCAGAATACTAGGGGACTATGGACCCCTACAGAACATC 660  
 Db 646 CTGGGGCATCCAGGGAGCAGAATACTAGGGGACTATGGACCCCTACAGAACATC 705  
 Qy 661 GCCAGGGAGGGAGTCAGGGGCTGAGGAACTTGGCCAACTATGAGGA 720  
 Db 706 GCCAGGGAGGGAGTCAGGGGCTGAGGAACTTGGCCAACTATGAGGA 765  
 Qy 721 GCTATGCTTAACTGTTGAGGTGGTGGCTTCAAGGAACTTCAGGAGACTCTGGAC 780  
 Db 766 GCTATGCTTAACTGTTGAGGTGGTGGCTTCAAGGAACTTCAGGAGACTCTGGAC 825  
 Qy 781 TACCACTGTCCTACTGACAACTTCCCTGCACTTGTCTGCTTGGAGCCGCTC 840  
 Db 826 TACCACTGTCCTACTGACAACTTCCCTGCACTTGTCTGCTTGGAGCCGCTC 885  
 Qy 841 TCTGCCACAGCTGCTCCGGGGAGCTGGTAAGAACGCCGTTATATGACTACT 900  
 Db 886 TCTGCCACAGCTGCTCCGGGGAGCTGGTAAGAACGCCGTTATATGACTACT 945  
 Qy 901 CGAGGCTGACTTCTGGCCCTCTGAGTGTGATAAGATGTGTCCTGGAGGGCCC 960  
 Db 946 CGAGGCTGACTTCTGGCCCTCTGAGTGTGATAAGATGTGTCCTGGAGGGCCC 1005  
 Qy 961 ACAGCCTTCTACAGGATTACCCCTTTCGGTTGGATCTCTGGACAGTGGTG 1020  
 Db 1006 ACAGCCTTCTACAGGATTACCCCTTTCGGTTGGATCTCTGGACAGTGGTG 1065  
 Qy 1021 ATGTCCTGAACTATGAGCTGAAAGGCGCTGATGAAAGTCCAGATGTACCGGA 1080  
 Db 1066 ATGTCCTGAACTATGAGCTGAAAGGCGCTGATGAAAGTCCAGATGTACCGGA 1125  
 Qy 1081 TCAAGGTTGAGAGGAGGAGGACTGGTAGCTAACCTGTCGAAACAGTAG 1140  
 Db 1126 TCAAGGTTGAGAGGAGGAGGACTGGTAGCTAACCTGTCGAAACAGTAG 1185  
 Qy 1141 ATGGAAG 1148  
 Db 1186 ATGGAAG 1193

RESULT 7  
 ID AAD30499  
 ID AAD30499 standard; cDNA; 1193 BP.

Qy 121 CCTCTAAAGGAGCTGGGAGGAGCTCCAGGAGTATGGTGAAGCTCAGCGT 180  
 Db 166 CCTCTAAAGGAGCTGGGAGGAGCTCCAGGAGTATGGTGAAGCTCAGCGT 225

AC ADD30499;  
 XX  
 DT 31-MAY-2002 (first entry)  
 XX  
 DE Human mitochondrial uncoupling protein 3 (UCP3) cDNA.  
 XX  
 KW Human; mitochondrial; uncoupling protein 3; UCP3; obesity; diabetes;  
 KW body weight disorder; gene therapy; chromosome 11q13; ss.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 199...1137  
 FT /\*tag= a /product= "Human UCP3 protein"  
 XX WO2002077554-A2.  
 XX PD 31-JAN-2002.  
 XX PP 25-JUL-2001; 2001WO-GB003341.  
 XX PR 25-JUL-2000; 2000GB-00018248.  
 XX PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX PI Clapham J;  
 DR WPI; 2002-217023/27.  
 DR P-PSDB; AAB19348.  
 XX PT Use of mitochondrial uncoupling protein 3 polypeptide, polynucleotide and  
 PT compounds which activate the polypeptide or polynucleotide for treating  
 PT obesity, diabetes or body weight disorder.  
 XX PS Claim 9; Page 18; 22pp; English.  
 XX CC The present sequence is human mitochondrial uncoupling protein 3 (UCP3)  
 CC encoding cDNA. The UCP3 gene is located on chromosome 11q13. UCP3  
 CC sequences are used for identifying compounds which modulate their  
 CC activity. They are used for the manufacture of a medicament for treating  
 CC obesity, diabetes and body weight disorder. UCP3 sequences are also used  
 CC in gene therapy.  
 XX SQ Sequence 1193 BP; 252 A; 369 C; 344 G; 228 T; 0 U; 0 Other;  
 Best Local Similarity 93.1%; Score 1146.4; DB 6; Length 1193;  
 Matches 1147; Conservative 99.9%; Pred. No. 3.3e-274;  
 Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 TCCTGGATGAGCCATTAGGAGGCCCTGCTGCCTCGTGCCTCGAGCTCACGCC 60  
 Db 46 TCCTGGATGAGCCATTAGGAGGCCCTGCTGCCTCGAGCTCACGCC 105  
 Qy 61 GCACCGTGCCTGAACGCCAGGTTAACCCCTCTTGGTTGGATCAAGAACCTGTG 120  
 Db 106 CCACCGTGCCTGAACGCCAGGTTAACCCCTCTTGGTTGGATCAAGAACCTGTG 165  
 Qy 121 CCCTAAAGGGCTGGCGAGAAGCTTCAGGACTATGGTGGCTGAGCTGAGGTG 180  
 Db 166 CCTTAAAGGGCTGGCGAGAAGCTTCAGGACTATGGTGGCTGAGCTGAGGTG 225  
 Qy 181 CCTCCGACCATGGCTGAAGTCCTGGGAGCAGGAGCAGGCTGTTCTGACCTC 240  
 Db 226 CCTCCGACCATGGCTGAAGTCCTGGGAGCAGGAGCAGGCTGTTCTGACCTC 285  
 Qy 241 GTTACCTTCAGTGGACAGCCAGTCCGCTCGAGTACAGGGAGAACCGGG 300  
 Db 286 GTTACCTTCAGTGGACAGCCAGTCCGCTCGAGTACAGGGAGAACCGGG 345  
 Qy 301 GTCCAGAGCGGCCGGCTGTGAGTACCGTGCCTGAGCTACCGTACCGT 360  
 Db 346 GTCCAGAGCGGCCGGCTGTGAGTACCGTGCCTGAGCTACCGTACCGT 405

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QY 361 CGGACTGAGGGTCCCTGAGCCCCCTACATGGCTGGAGCCAGCTGAGCGCAGATG 420  
 Db 406 CGACTGAGGTCCCTGAGGCCCTACATGGCTGGAGCCAGCTGAGCGCAGATG 465  
 QY 421 AGCTTGCCCTACATCCGCTAGGCTCTTGTAGCTCGTCAAGCAGGTGTAACCCCCAA 480  
 Db 466 AGCTTGCCCTACATCCGCTAGGCTCTTGTAGCTCGTCAAGCAGGTGTAACCCCCAA 525  
 QY 481 GCGCGGACAATCCGCTCACTACCCGATTGCGGGTCACACAGGGCCATG 540  
 Db 526 GGCAGGACACTCAGCTACTACCCGATTGCGGGTCACACAGGGCCATG 585  
 QY 541 GCGGAGCCCTGAGGAGCCAGATGGCTGGAGGCTGAGCTACAGGACATAC 600  
 Db 586 GCGGAGCCCTGAGGAGCCAGATGGCTGGAGGCTGAGCTACAGGACATAC 645  
 QY 601 CTGGGGCATCCAGGAGCAGGAGCAGAATAACAGCGAGCATAGGGCTACAGAACATC 660  
 Db 646 CTGGGGCATCCAGGAGCAGGAGCAGAATAACAGCGAGCATAGGGCTACAGAACATC 705  
 QY 661 GCGGAGGAGGAGAGCTGAGGCTGAGGAGCAGGAGCTGAGGAGCTGAGGAGCT 720  
 Db 706 GCGGAGGAGGAGAGCTGAGGCTGAGGAGCAGGAGCTGAGGAGCTGAGGAGCT 765  
 QY 721 GCTATGTCACTGGCTGGAGGTGACTGACCTACAGGAGCTGAGGAGCTGAGGAGCT 780  
 Db 766 GCTATGTCACTGGCTGGAGGTGACTGACCTACAGGAGCTGAGGAGCTGAGGAGCT 825  
 QY 781 TACCACTGCTCACTGAACACTCCCTGCACTTGTCTCTGCCTTGAGGCCGCTC 840  
 Db 826 TACCACTGCTCACTGAACACTCCCTGCACTTGTCTCTGCCTTGAGGCCGCTC 885  
 QY 841 TGTGACCACTGGTGCCTCCCGCTGAGGCTGGTGAAGAACCTGACTCACC 900  
 Db 886 TGTGACCACTGGTGCCTCCCGCTGAGGCTGGTGAAGAACCTGACTCACC 945  
 QY 901 CCAGGCGAAGTCACTGGCCCTGACTGATGATAAGTGGGCCCGAGGAGCTGAGC 960  
 Db 946 CCAGGCGAAGTCACTGGCCCTGACTGATGATAAGTGGGCCCGAGGAGCTGAGC 1005  
 QY 961 ACAGCTCTACACGGATTACACCCCTTTGGTTGGATCAAGATGGAGCTCTGGAC 1020  
 Db 1006 ACAGCTCTACACGGATTACACCCCTTTGGTTGGATCAAGATGGAGCTCTGGAC 1065  
 QY 1021 ATGTCGTGAACTATGAGCAGCTGAACTGGCCCTGATGAAAGTCAGTGTACGGAA 1080  
 Db 1066 ATGTCGTGAACTATGAGCAGCTGAACTGGCCCTGATGAAAGTCAGTGTACGGAA 1125  
 QY 1081 TCACCTTGTACAGACAGAGGCCACTGGTGGCTAACGTTGGCAACCCATTAAG 1140  
 Db 1126 TCACCTTGTACAGACAGACAGAGGCCACTGGTGGCTAACGTTGGCAACCCATTAAG 1185  
 QY 1141 AATGGAG 1148  
 Db 1186 ATGGAG 1193

RESULT 8  
 AAZ29245  
 ID AAZ29245 standard; cDNA; 1175 BP.  
 XX  
 AC AAZ29245;  
 XX  
 DT 28-FEB-2000 (first entry)  
 XX  
 DE Human mitochondrial anion carrier, uncoupling protein-3 cDNA.  
 XX  
 KW Mitochondrial uncoupling protein-3; UCP-3; mitochondrial anion carrier;  
 KW MAC; modulator; transport protein; fatty acid anion; mitochondria;  
 KW assay vesicle; metabolic disorder; diabetes; obesity; cancer; human; de.  
 XX  
 OS Homo sapiens.

XX  
 FH  
 KEY  
 FT  
 CDS  
 FT  
 /product= "UCP-3"  
 XX  
 WO9964458-A1.  
 XX  
 PD  
 16-DEC-1999.  
 XX  
 PT  
 08-JUN-1999; 99WO-US012623.  
 XX  
 PR  
 08-JUN-1998; 98US-00093662.  
 XX  
 PA  
 (UYBO-) UNIV BOSTON.  
 XX  
 PT  
 CORKEY BR, Hamilton JA, Pilch PF, Farmer SR, Kirkland JL;  
 DR  
 P-PSDB; AAY44253.  
 XX  
 PT  
 Identifying modulators of mitochondrial anion carriers, potentially useful for treating metabolic disease, e.g. diabetes and obesity.  
 XX  
 PS  
 Claim 11; Page 72-3; 8pp; English.  
 XX  
 CC  
 3) which is a mitochondrial anion carrier (MAC). The UCPs transport free fatty acid anions across the inner mitochondrial membrane to induce cyclical proton movement. This transport is tightly related to oxidation of fatty acids in the mitochondria, thereby converting fatty acids into energy rather than storing them. The uncoupling protein is used in the preparation of assay vesicles that are used to identify modulators of MAC activity. MAC modulators are useful for treating metabolic disorders, particularly diabetes and obesity. Modulators that act as inhibitors, can be used to treat conditions requiring a reduction in energy expenditure, e.g. in cancer patients or the elderly  
 XX  
 Sequence 1175 BP; 248 A; 362 C; 337 G; 228 T; 0 U; 0 Other;  
 Query Match 93.0%; Score 1145; DB 3; Length 1175;  
 Best Local Similarity 100.0%; Pred. No. 7.3e-274;  
 Matches 1145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 SQ  
 1 TCTGGGATGGGCCCTAGGGGCCCTGTGCGCTTGAGGACTCACAGCC 60  
 QY  
 31 TCTGGGATGGGCCCTAGGGGCCCTGTGCGCTTGAGGACTCACAGCC 90  
 DB  
 61 CCACCGCTGCAGTGAAGGCCAGGGCTTGAGCAGCAGCTCTCTCTTGAGCCCTCTCGG 120  
 QY  
 91 CCACCGCTGCAGTGAAGGCCAGGGCTTGAGCAGCAGCTCTCTCGG 150  
 DB  
 121 CCTAAAGGGACTGGCAGAAGCTTCAGGAGTATGGTGTGAGCTTCAGAGTG 180  
 DB  
 151 CCTAAAGGGACTGGCAGAAGCTTCAGGAGTATGGTGTGAGCTTCAGAGTG 210  
 QY  
 181 CCTCCCCACCATGCTGTGAGTCTCTGGGGAGGCAAGGGCTTTCTGACCTC 240  
 DB  
 211 CCTCCCCACCATGCTGTGAGTCTCTGGGGAGGCAAGGGCTTTCTGACCTC 270  
 QY  
 241 GTTACCTTCCACTGGACACGCCAACGGCTCCCTGAGATCAGGGAGAACGGG 300  
 DB  
 271 GTTACCTTCCACTGGACACGCCAACGGCTCCCTGAGATCAGGGAGAACGGG 330  
 QY  
 301 GTTACCTTCCACTGGACACGCCAACGGCTCCCTGAGATCAGGGAGAACGGG 360  
 DB  
 331 GTTACCTTCCACTGGACACGCCAACGGCTCCCTGAGATCAGGGAGAACGGG 390  
 QY  
 361 CGGACTGAGGGCTCTGAGCCCTACATGGCTGTGAGCTTCAGGGTAG 420  
 DB  
 391 CGGACTGAGGGCTCTGAGCCCTACATGGCTGTGAGCTTCAGGGTAG 450  
 QY  
 421 ACTTCCTCCATCCGATCGCCCTATGACTCCCTCACAGCAGGTGACCCCCAA 480

Db  
 451 AGCTTGGCCATCCATCCGATCGCCCTATGACTCCCTCACAGCAGGTGACCCCCAA 510  
 Qy  
 481 GGCGGGAGAACCTACGGCTCACTACCCGGATTGGCGCGCTGACCCAGGGATG 540  
 Db  
 511 GGGGGAGAACCTACGGCTCACTACCCGGATTGGCGCGCTGACCCAGGGATG 570  
 Qy  
 541 GCGGGACTGTGCCAGGCCACAGATGGTGGAGGTCGATTCAGCCAGGATAC 600  
 Db  
 571 GCGGTAACCTGTGCCAGGCCACAGATGGTGGAGGTCGATTCAGCCAGGATAC 630  
 Qy  
 601 CTCGGGCCATCAGGGACACAGAAATTCAGGGACTATGGAGGCTACAGGACCTC 660  
 Db  
 631 CTGGGGCCATTCAGGGACACAGAAATTCAGGGACTATGGAGGCTACAGGACCTC 690  
 Qy  
 661 GCCAGGGAGAGGTGGGGCTGTTGAGAAGGAACCTTGCCACATCATGAGGA 720  
 Db  
 691 GCCAGGGAGAGGTGGGGCTGTTGAGAAGGAACCTTGCCACATCATGAGGA 750  
 Qy  
 721 GCTATCGTCACTGTGCTAGGGTGTGACTACCATCTCGGAGGAGCTTGCC 780  
 Db  
 751 GCTATCGTCACTGTGCTAGGGTGTGACTACCATCTCGGAGGAGCTTGCC 810  
 Qy  
 781 TACACCTGTCACTGACACTTCCTGCACTTGTTCTGCTTSGAGCCGCTC 840  
 Db  
 811 TACACCTGTCACTGACACTTCCTGCACTTGTTCTGCTTSGAGCCGCTC 870  
 Qy  
 841 TGTGCCACAGTGGTGGCTCCCGGGTGGAGCTGTTGTTCTGCTTSGAGCCGCTC 900  
 Db  
 871 TGTGCCACAGTGGTGGCTCCCGGGTGGAGCTGTTGTTCTGCTTSGAGCCGCTC 930  
 Qy  
 901 CCAGGCGACTTCTGGCCCTCACTGTTGATGATAAAGTGGAGCCAGGAGCCC 960  
 Db  
 931 CCAGGCGACTTCTGGCCCTCACTGTTGATGATAAAGTGGAGCCAGGAGCCC 990  
 Qy  
 961 ACAGCCTTCTACAAGGGATTACACCTCTTGGCTTGGATGAGTGGTGGAGCTG 1020  
 Db  
 991 ACAGCCTTCTACAAGGGATTACACCTCTTGGCTTGGATGAGTGGTGGAGCTG 1050  
 Qy  
 1021 ATGTTGTTAATCTATGAGCAGCTGAGAACGGCCCTATGAGAAGTCCAGATTTACGGAA 1080  
 Db  
 1051 ATGTTGTTAATCTATGAGCAGCTGAGAACGGCCCTATGAGAAGTCCAGATTTACGGAA 1110  
 Qy  
 1141 AATGG 1145  
 Db  
 1171 AATGG 1175

RESULT 9  
 AAV54602  
 ID AAV54602 standard; cDNA; 1193 BP.  
 XX  
 AC  
 AAV54602;  
 XX  
 DT  
 07-DEC-1998 (first entry)  
 XX  
 DE Human uncoupling protein HNFCM60 cDNA.  
 XX  
 KW HNFCM60; uncoupling protein; human; body weight disorder; obesity;  
 KW diabetes; hyperlipidaemia; diagnosis; therapy; vaccine; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FT  
 Key  
 CDS  
 /\*tag= a  
 PN WO9839432-A1.  
 XX  
 Location/Qualifiers  
 199. .1137  
 FT  
 FT  
 PN WO9839432-A1.

11-SEP-1998. XX  
 02-MAR-1998; 98WO-GB000633.  
 PR 05-MAR-1997; 97GB-00004551.  
 PR 18-MAR-1997; 97GB-00005654.  
 PR 16-JUL-1997; 97EP-0030505.  
 XX  
 PA (SMK) SMITHKLINE BEECHAM PLC.  
 XX  
 PI Beeley LJ, Paine K, Golden RJ;  
 XX  
 DR WPI: 1998-49584142.  
 DR P-PSDB; AAW68197.  
 XX  
 PT New isolated human uncoupling poly:peptide(s) - used to develop products for the diagnosis, prevention and treatment of body weight disorders, obesity and diabetes.  
 PT XX  
 PS Claim 3; Page 24-25; 41p; English.  
 XX  
 CC This isolated polynucleotide (PN) codes for novel human uncoupling protein HNFCW60 (see AAW68197). HNFCW60 polynucleotides (see also AAV5-04) can be obtained from a cDNA derived from mRNA in cells of human brain frontal cortex, rhabdomyosarcoma, foetal heart and skeletal muscle using expressed sequence tag analysis. The invention relates to HNFCW60 polypeptides and recombinant materials and methods for their production. It also relates to methods for using such HNFCW60 polypeptides and polynucleotides. Such uses include the treatment of obesity, diabetes, hyperlipidaemia and body weight disorders. The invention also provides methods to identify agonists and antagonists, and methods for treating conditions associated with HNFCW60 imbalance using the identified compounds. In addition, diagnostic assays for detecting diseases associated with inappropriate HNFCW60 activity or levels are provided  
 CC XX  
 SQ Sequence 1193 BP; 252 A; 370 C; 343 G; 228 T; 0 U; 0 other;  
 Query Match 93.0%; Score 1144.8; DB 2; Length 1193;  
 Best Local Similarity 99.8%; Pred. No. 8.2e-274; Matches 1146; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 TCCCTGGGAGGCCCTAGGGAGGCCCTGCGGCCCTCGGCGAGACTCAAGCC 60  
 Db 46 TCTCTGGATAGGCTCTAGGAGCCCTGCTCCCTCCCTGGACCTCTCAGCC 105  
 Qy 61 CCACCGCTGCACTGAGCCAGGCTGTGAGCAGGACCTCTCTGGACCTCTCTCG 120  
 Db 105 CCACCGCTGCACTGAGCCAGGCTGTGAGCAGGACCTCTCTCTCG 165  
 QY 121 CCTTAAGGACTGGCAGAGCTTCCAGACTATGGTGACTGAACTTCAGACGG 180  
 Db 166 CCTTAAGGACTGGCAGAGCTTCCAGACTATGGTGACTGAACTTCAGACGG 225  
 QY 181 CCTCCACCATGGCTGTGAGTTCTGGGGCAGCACAGCAGCTGTTGCTGACCTC 240  
 Db 226 CCTCCACCATGGCTGTGAGTTCTGGGGCAGCACAGCAGCTGTTGCTGACCTC 285  
 QY 241 GTTACCTTCCACTGAGCACAGCCAGGTCTGGCTCGCTGAACTCCAGGGAGA 300  
 Db 286 GTTACCTTCCACTGAGCACAGCCAGGTCTGGCTCGCTGAACTCCAGGGAGA 345  
 QY 301 GTCCGAGCAGCCGAGTCAGGCTGAGCTGGCTGTGAGCTGGCTGAGCTGG 360  
 Db 346 GTCCGAGCAGCCGAGTCAGGCTGAGCTGGCTGTGAGCTGGCTGAGCTGG 405  
 QY 361 CGGACTGAGCTGGTCTCCATCGACGACGAGCTGAGCTGGCTGAGCTGG 420  
 Db 406 CGGACTGAGCTGGTCTCCATCGACGACGAGCTGAGCTGGCTGAGCTGG 465  
 QY 421 AGCTTGCCCTCATCGACGAGCTGAGCTGGCTGAGCTGGCTGAGCTGG 480  
 Db 466 AGCTTGCCCTCATCGACGAGCTGAGCTGGCTGAGCTGGCTGAGCTGG 525  
 QY 481 GGCGGGGACACTCCAGCTTCACTACCCGATTGCGGGCTGACCGAGGACCATG 540  
 Db 526 GGCGGGACACTCCAGCTTCACTACCCGATTGCGGGCTGACCGAGGACCATG 585  
 QY 541 GGGTGAACCTGTGCCAGCCAGATGTTGGAGTCGATTTCAGCCAGCATAC 600  
 Db 586 GGGTGAACCTGTGCCAGCCAGATGTTGGAGTCGATTTCAGCCAGCATAC 645  
 QY 601 CTCCGGCCATTCAGAGGAGGAGAAATAGCGGGACTATGGACGCCATAC 660  
 Db 646 CTCCGGCCATTCAGAGGAGGAGAAATAGCGGGACTATGGACGCCATAC 705  
 QY 661 GCCGGGAGGAGAGTCAAGGGCTGAGTGAAGGAACTTGCCAAACATACTGAGGAAT 720  
 Db 706 GCCAGGGAGGAGGTGAGGGCTGAGTGAAGGAACTTGCCAAACATACTGAGGAAT 765  
 QY 721 GCTATGTCACAGTGCTGAGGTTGACTGACATCCAGAGAACGCTGAC 780  
 Db 766 GCTATGTCACAGTGCTGAGGTTGACTGACATCCAGAGAACGCTGAC 825  
 QY 781 TACCACTCTACTGACACTTCCCTACACTTGTCTGCTCTGGCGCGCTC 840  
 Db 826 TACCACTCTACTGACACTTCCCTACACTTGTCTGCTCTGGCGCGCTC 885  
 QY 841 TGTGCACTGGGACCTCCCGTGGACTGTTGAGGAACTGACTCACC 900  
 Db 886 TGTSACAGTGGTACCTCCCGTGGACTGTTGAGGAACTGACTCACC 945  
 QY 901 CCAGGCCAGTACTGAGCCCTCACTGATGATAAGATGGTGGCCAGAGGCCCC 960  
 Db 946 CCAGGCCAGTACTGAGCCCTCACTGATGATAAGATGGTGGCCAGAGGCCCC 1005  
 QY 961 ACASCTCTTACAGGGATTACCCCTTTGGCTGGAACTGGTGG 1020  
 Db 1006 ACASCTCTTACAGGGATTACCCCTTTGGCTGGAACTGGTGG 1065  
 QY 1021 ATGTTGTACTTACGGCTGAAACGGGCCCTGATGAACTGGCTGAGTTACGGAA 1080  
 Db 1066 ATGTTGTACTTACGGCTGAAACGGGCCCTGATGAACTGGCTGAGTTACGGAA 1125  
 QY 1081 TCACCGTTGAGACAGAGAAAGGCCACTGTGAGCTAAGCTGGTGGCGAGAACCTGTA 1140  
 Db 1126 TACCGTTGAGACAGAGAAAGGCCACTGGTACCTAAGCTGGTGGCGAGAACCTGTA 1185  
 QY 1141 ATGGRAG 1148  
 Db 1186 ATGGRAG 1193  
 RESUIT 10  
 AAX08507  
 ID AAX08507 standard; DNA; 1022 BP.  
 XX  
 AC AAX08507;  
 XX  
 DT 19-JUL-1999 (first entry)  
 XX  
 DB Human UCP-3 (uncoupling protein) gene.  
 XX  
 KW UCP-3; uncoupling protein; thermogenesis; skeletal muscle; treatment; obesity; diabetes; hyperthermia; fever; detection; diagnosis; ss.  
 KW Homo sapiens.  
 FH Key CDSS  
 FT Location/Qualifiers  
 FT 28..966  
 FT /\*tag= a  
 FT /product= "Uncoupling protein"  
 PN WO9845313-A1.  
 XX  
 PD 15-OCT-1998.

XX	PF	25-MAR-1998;	98WO-US00592.
PR	04-APR-1997;	97US-0043407P.	
PR	08-MAY-1997;	97US-0046154P.	
XX	PA	(AMYL-) AMYLIN PHARM INC.	
XX	PI	Larkin S, Moore C, Albrandt K, Young A, Beaumont K;	
XX	WPI:	1999-131682/11.	
DR	P-PSDB:	AAW8567.	
XX	PT	New isolated uncoupling protein, UCP3 - used to develop products for modulating thermogenesis in tissues, e.g. for treating obesity, diabetes, malignant hyperthermia or fever.	
PS	Claim 5; Fig 5; 97pp; English.		
XX	CC	The uncoupling protein UCP-3 is involved in thermogenesis and energy utilization in skeletal muscle. The nucleic acid molecule encoding UCP-3 or compounds which activate UCP-3 can be used to increase thermogenesis in a subject, e.g. for treating obesity or for decreasing the amount of fat in a subject. They can also be used for treating diabetes. Compounds which inhibit UCP-3 activation in tissues of a subject can be used for decreasing thermogenesis or respiratory ATP synthesis, e.g. for preventing or treating malignant hyperthermia or fever. The UCP-3 can also be used for screening for compounds that bind to or modulate the activity of UCP-3, these compounds can then be used in detection and diagnosis	
XX	SQ	Sequence 1022 BP; 228 A; 301 C; 292 G; 201 T; 0 U; 0 Other;	
Query	Match	82.1%; Score 1010.8; DB 2; length 1022;	
Best	Local Similarity	99.8%; Pred. No. 1.3e-240;	
Matches	1012; Conservative	0; Mismatches 2; Indels 0; Gaps 0;	
OY	135	GGCGAGGCTTCAGGACTATGGTTGACTGAACCTCAGAGGTGCTCCACATGCC	
Db	9	GCGAGGACTTCAGGACTATGGTTGACTGAACCTCAGAGGTGCTCCACATGCC	
OY	195	TGTCAAGTTCCTGGGGAGGACAGACAGAACCGCTGTTGACTGACCTCGTACCT	
Db	69	TGTCAAGTTCCTGGGGAGGACAGACAGAACCGCTGTTGACTGACCTCGTACCT	
OY	255	GGACACSCCAAGTGTCTGCAGATCCAGGGAGGACAGCGGGCTCATCTGACCATGGGACTGAGGTTCC	
Db	129	GGACACSCCAAGTGTCTGCAGATCCAGGGAGGACAGCGGGCTCATCTGACCATGGGACTGAGGTTCC	
OY	315	GCTGGTGAGTACGGGGGGCTGGGACCATCTGACCATGGGACTGAGGTTCC	
Db	189	GCTGGTGAGTACGGGGGGCTGGGACCATCTGACCATGGGACTGAGGTTCC	
OY	375	CTSGAGCCCTACATAGGCTGGGGCCGCCTAACAGCCAGATGAGCTTCCTCCAT	
Db	249	CTGGAGCCCTACATAGGCTGGGGCCGCCTAACAGCCAGATGAGCTTCCTCCAT	
OY	435	CCGCATCGCCTCTATGCTCCGAAACAGGTTGACCCCAAAGGGCGCACACTC	
Db	309	CCGCATCGCCTCTATGCTCCGAAACAGGTTGACCCCAAAGGGCGCACACTC	
OY	495	CAGGCTCACTACCGGATTGGGGCTGGCACACAGGGCTGGGGTACCTGTC	
Db	369	CAGGCTCACTACCGGATTGGGGCTGGCACACAGGGCTGGGGTACCTGTC	
OY	555	CCAGCCCACAGATGGTGAAGGTCGATTTCAGGCCAGCATCACCTCGGGCATCCAG	
Db	429	CCAGCCCACAGATGGTGAAGGTCGATTTCAGGCCAGCATCACCTCGGGCATCCAG	
OY	615	GACGGACGAAATACTACGGGACTATGCGCTACAGAACCTGCGGAGGAGG	
Db	489	GACGGACGAAATACTACGGGACTATGCGCTACAGAACCTGCGGAGGAGG	
OY	675	AGTCAGGGGCTGTGAGAAGGACTTGCCACACATGAGGAAATGTTCACTG	
XX	RESULT	11	
ID	AAV72691	standard; cDNA; 1132 BP.	
XX	AC	AAV72691;	
XX	DT	22-FEB-1999 (first entry)	
XX	DE	Human uncoupling protein UCP3S encoding cDNA.	
KW	Human; uncoupling protein; UCP3L; UCP3S; oxidative phosphorylation; adenosine triphosphate; mitochondria; skeletal muscle; gene therapy; thermogenesis; heart; obesity; cachexia; type II diabetes; hypertension; insulin sensitivity; neuromuscular disease; ss.		
XX	OS	Homo sapiens.	
XX	PH	Location/Qualifiers	
CD	Key	154..991	
PT	CD	/*tag= a	
FT		/product= "UCP3S"	
XX	PN	WO9850542-A1.	
XX	PD	12-NOV-1998.	
XX	PF	05-MAY-1998; 98WO-EP002645.	
XX	PR	07-MAY-1997; 97CH-00001072.	
XX	PA	(NOV) NOVARTIS AG.	
PA	(NOV) NOVARTIS ERFINDUNGEN VERW GES MBH.		
PI	Giacobino J, Muzzin P, Boss O;		
XX	DR	WPI, 1998-610382/51.	
DR	P-PSDB;	AAW83380.	
XX	PT	New human skeletal muscle uncoupling proteins UCP3L and UCP3S - useful for controlling thermogenesis in human skeletal muscle and heart, e.g. for treating obesity and cachexia.	

XX  
 PS Claim 3; Page 17-18; 26pp; English.  
 XX  
 CC The present sequence encodes human uncoupling protein UCP3S. UCP3  
 CC unouples oxidative phosphorylation and synthesis of adenosine  
 CC triphosphate in the mitochondria of skeletal muscle. The coding sequences  
 for UCP3L and UCP3S are useful for gene therapy of dysfunctions of  
 thermogenesis in human skeletal muscle and heart which result from a lack  
 of UCP3 and which can induce disorders such as obesity or cachexia.  
 CC Antisense oligonucleotides to UCP1 and UCP3S can be used for correcting  
 an excess of UCP3. Modification of endogenous UCP3 activity (using  
 activators or inhibitors of UCP3) is used to induce bodyweight loss (loss  
 of adipose mass and maintenance of the lean mass) in all types of obesity  
 by promoting the dissipation of energy; for preventing an excessive  
 weight regain following restrictive food diet or after ceasing a physical  
 training programme; for preventing and treating type II diabetes by  
 improving sensitivity to insulin; for preventing hypertension; for  
 increasing muscle mass in states of cachexia; for treatment of  
 insufficiencies or disturbances of cardiac rhythm due to a dysfunction of  
 UCP3; and for the treatment of neuromuscular diseases due to a  
 dysfunction of UCP3. The uncoupling proteins can also be used to raise  
 antibodies, e.g. for diagnosis. Knowledge of the UCP3 genes allows  
 generation of transgenic animals, e.g. for screening substances which  
 modulate UCP3 expression or activity or for investigating the biological  
 role of UCP3  
 CC  
 XX Sequence 1132 BP; 245 A; 351 C; 321 G; 215 T; 0 U; 0 Other;  
 SQ

Query Match 79.7%; Score 981.4; DB 2; Length 1132;  
 Best Local Similarity 99.4%; Pred. No. 2-e-233;  
 Matches 985; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TCTCTGGATGAGGCCCTTGGAGGAGCCCTGCGCCCTSGGTGAGGTACAGCC 60  
 Db 1 TCTCTGGATGAGGCCCTTGGAGGAGCCCTGCGCCCTGCGTGGAGGTACAGCC 60  
 QY 61 CCACCGCTGACTGAGGCCCTGGAGGAGCCCTGCGTGGAGGTACAGCC 60  
 Db 61 CCACCGCTGACTGAGGCCCTGGAGGAGCCCTGCGTGGAGGTACAGCC 60  
 QY 121 CCTAAAGGGACTGGGAGAGCCTTCAGGACTATGGTGAAGCTGAGGCTTCAGAGTG 180  
 Db 121 CCTAAAGGGACTGGGAGAGCCTTCAGGACTATGGTGAAGCTGAGGCTTCAGAGTG 180  
 QY 181 CCTCCCAACCATGGCTGAAATTCCTGGGGAGGGACAGAACGCTGTTTGTGACCTC 240  
 Db 181 CCTCCCAACCATGGCTGAAATTCCTGGGGAGGGACAGAACGCTGTTTGTGACCTC 240  
 QY 241 GTTACCTTCACTGGACACGCCAGGTCCCTCGAGTCAGGGAGAACCGGG 300  
 Db 241 GTTACCTTCACTGGACACGCCAGGTCCCTCGAGTCAGGGAGAACCGGG 300  
 QY 301 GTTACCTTCACTGGACACGCCAGGTCCCTCGAGTCAGGGAGAACCGGG 360  
 Db 301 GTTACCTTCACTGGACACGCCAGGTCCCTCGAGTCAGGGAGAACCGGG 360  
 QY 361 CGACTGAGGGCCCTTGAGCCCTAGATGGCTGGGGCTGAGGTACAGGAGATG 420  
 Db 361 CGACTGAGGGCCCTTGAGCCCTAGATGGCTGGGGCTGAGGTACAGGAGATG 420  
 QY 421 AGCTTGCTCATTCGCATTCGCTTGTGAGGTCCCTGAGGTACAGGAGATG 480  
 Db 421 AGCTTGCTCATTCGCATTCGCTTGTGAGGTCCCTGAGGTACAGGAGATG 480  
 QY 481 GGGGGGAACTTCGCTTGTGAGGTCCCTGAGGTACAGGAGATG 540  
 Db 481 GGGGGGAACTTCGCTTGTGAGGTCCCTGAGGTACAGGAGATG 540  
 QY 541 GGGGGAACTTCGCTTGTGAGGTCCCTGAGGTACAGGAGATG 600  
 Db 541 GGGGGAACTTCGCTTGTGAGGTCCCTGAGGTACAGGAGATG 600  
 QY 601 CTGGGGCATCCAGGAGGAGAAGATAACGGGGACTATGGACGCCATACAGAACCTC 660

RESULT 12  
 AAZZ2324 standard; cDNA; 1132 BP.  
 ID AAZZ2324  
 XX  
 AC AAZZ2324;  
 DT 29-FEB-2000 (first entry)  
 XX  
 DE Human uncoupling protein-3S cDNA.  
 KW Human uncoupling protein-3S; UCP; immune response; electron transport;  
 KW oxidative phosphorylation; Major histocompatibility complex;  
 KW MHC class I HLA-DR; proton motor force; mitochondrial membrane potential;  
 KW mitochondrial metabolism; cancer; autoimmune disease;  
 KW neurodegenerative disorder; db.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key  
 FT CDS  
 FT /\*tag= "Human uncoupling protein-3S"  
 FT /product= "Human uncoupling protein-3S"  
 DN W0953953-A2.  
 XX  
 PD 28-OCT-1999.  
 XX  
 PR 30-MAR-1999; 99WO-US006974.  
 XX  
 PR 17-APR-1998; 98US-0082250P.  
 PR 29-JUL-1998; 98US-0094519P.  
 PR 24-SEP-1998; 98US-0101588P.  
 XX  
 PA (UYVB-) UNIV VERMONT.  
 XX  
 PT Newell MK;  
 XX  
 DR WPI; 2000-096773/08.  
 DR P-PSDB; AAY44293.  
 XX  
 PT Use of cell surface and membrane characteristics for developing products  
 PT for treating cancers, autoimmune diseases or neurodegenerative diseases.  
 XX  
 Disclosure; Page 119-120; 123pp; English.

QY	841	TGTGCCACAGTGGCCCTCCCCGGTGGCTGAGGCGCCGTTATGACTCACCCT	900
Db	841	TGTGCCACAGTGGCTGAGGCGCCGTTATGACTCACCCT	900
Qy	901	CCAGGCGAGTCTTGCCCTCTGAGCTGTTGAGGCGCCGTTATGACTCACCCT	960
Db	901	CCAGGCGAGTCTTGCCCTCTGAGCTGTTGAGGCGCCGTTATGACTCACCCT	960
Qy	961	ACAGCTTCCTACAAGGGATTACACCTCT	991
Db	961	ACAGCTTCCTACAAGGGATTACACCTCT	991
RESULT 13			
ID	AAS14820	standard; cDNA; 1132 BP.	
XX			
AC	AAS14820;		
XX			
DT	13-DEC-2001	(first entry)	
XX			
DE	Human cDNA encoding partial UCP-3S protein.		
XX			
KW	Human; Uncoupling protein; UCP-3S; ss: transgenic plant; fuel metabolism; antibacterial; bacterial infection; environmental stress; food.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	127..981	
FT	/*tag	&	
FT	/product	= "UCP-3S"	
FT	/partial		
FT	/note	= "No start codon"	
XX			
PN	W020175131-A2.		
XX			
PD	11-OCT-2001.		
XX			
PF	30-MAR-2001; 2001WO-US010236.		
XX			
PR	31-MAR-2000; 2000US-019333P.		
XX			
PA	(UTYB-) UNIV TECHNOLOGY CORP.		
XX			
PI	Berry-Lowe SL, Newell MK;		
XX			
DR	WPI; 2001-036442/72.		
XX			
PT	Plants expressing heterologous cell-wall uncoupling protein, have altered metabolism, resistance to infection and stress sensitivity.		
XX			
PS	Disclosure; Page 60-61; 72pp; English.		
XX			
CC	The invention relates to a transgenic plant expressing a cell-wall UCP (uncoupling protein) encoded by a heterologous gene. The heterologous UCP, when expressed in the plant cell wall, plasma membrane or chloroplast regulates the fuel metabolism of the plant. Regulating expression or activity of UCP is used to control fuel metabolism.		
CC	especially reducing UCP expression produces nutritionally improved plants and protects against infection e.g. bacterial, while decreasing UCP expression improves sensitivity to light and cold. Altering UCP activity can improve crop productivity and durability towards environmental stress, and it eliminates time-consuming and expensive maintenance and repetitive application of chemicals. The present sequence encodes human UCP -3S and is used as the heterologous UCP in the method of the invention		
CC	Sequence 1132	BP; 245 A; 351 C; 321 G; 215 T; 0 U; 0 Other;	
XX			
Query Match	79.7%	Score 981.4; DB 5; Length 1132;	
Best Local Similarity	99.4%	Pred. No. 2.7e-2233;	



KW glucokinase; hepatic triglyceride accumulation; fibrinogen; HDL; KRW fatty acid oxidation; high density lipoprotein; cholesterol; KRW glucose; gestational diabetes; hyperglycaemic related disorder; kidney related disorder; cardiovascular disorder; gene; sB.  
 KW XX Unidentified.

XX PH Location/Qualifiers  
 PT 154 - .981  
 FT /\*tag= a  
 FT /product= "UCP3S protein"

XX PN US2002065239-A1.  
 XX PD 30-MAY-2002.  
 XX PP 14-MAR-2001; 2001US-00808457.  
 XX PR 15-MAR-2000; 2000US-0266328P.  
 XX PA (CAPL/)  
 PA CAPLAN S. L.  
 PA (BOET/)  
 PA BOETTCHER B. R.  
 PA (SLOS/)  
 PA SLOSBERG E. D.  
 PA (CONN/)  
 PA CONNELLY S.  
 PA (KALE/)  
 PA KALEKO M.  
 PA (DESA/)  
 PA DESAI U. J.  
 XX PI Caplan SL, Boettcher BR, Slosberg ED, Connely S, Kaleko M;  
 PI Desai UJ;  
 DR DR PPI; 2002-556735/59.  
 XX DR P-PSDB; ABB81611.

XX PT Treating condition related to elevated blood glucose levels, especially diabetes or obesity, involves administering polynucleotide sequence PT encoding glucokinase regulatory protein, to a subject.

XX DS Disclosure; Page 17-18; 42pp; English.

The present invention describes a method (M1) for treating a condition related to elevated blood glucose levels, which involves administering a polynucleotide sequence encoding a glucokinase regulatory protein (GKRP), to a subject. Also described: (1) increasing liver glucokinase (GK) activity, by administering a polynucleotide sequence encoding GKRP; and (2) a method (M2) treating diabetes or diabetes-related condition, by administering to a subject, one or more metabolism modifying proteins and peptides in combination with GK or GKRP, or their combination. (M1) and (M2) can be used for treating diabetes (type I and II diabetes) or diabetes-related conditions such as obesity, increased hepatic triglyceride accumulation, reduced hepatic fatty acid oxidation, increased fibrinogen levels, decreased apo A-I levels, decreased high density lipoprotein (HDL) cholesterol levels and decreased hepatic glucose utilization. The methods are also useful for treating gestational diabetes, hyperglycemic related disorders such as increased cholesterol, kidney related disorders and cardiovascular disorders. The methods usually increases liver size and hepatic fat accumulation in normal and diabetic mice. The present sequence encodes a UCP3S protein which is given in the exemplification of the present invention

XX Sequence 1132 BP; 245 A; 351 C; 321 G; 215 T; 0 U; 0 Other;

Query Match 79.7%; Score 981.4; DB 6; Length 1132;  
 Best Local Similarity 99.4%; Pred. No. 2.7e-233;  
 Matches 985; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

XX DT 1 TCCTGGATGAGGCCCTGAGCCCTGTGAGCTCGCCCTGCCTGAGCTCACAGCC 60  
 DB 1 TCTGGATGGAGCCCTGAGCCCTGTGAGCTCGCCCTGCCTGAGCTCACAGCC 60

XX DT 61 CCACCGTCACTGAACCCGAGGCTGAGACGACCTCTCTCTGAGCTCTCGG 120  
 DB 61 CCACCGTCACTGAACCCGAGGCTGAGACGACCTCTCTCTGAGCTCTCGG 120

Db UCP3S cDNA clone nucleotide sequence.

XX UCP3L; UCP3S; diabetes; obesity; diabetic related condition; GKRP; KW gene therapy; antidiabetic; anorectic; cardiotropic; nephrotropic; GK; KW anti-lipaemic; blood glucose; glucokinase regulatory protein; liver;

RESULT 15

ABQ73000

ABQ73000 standard; cDNA; 1132 BP.

AC ABQ73000;

XX 20-SEP-2002 (first entry)

XX DE

XX UCP3S cDNA clone nucleotide sequence.

XX UCP3L; UCP3S; diabetes; obesity; diabetic related condition; GKRP;

KW gene therapy; antidiabetic; anorectic; cardiotropic; nephrotropic; GK; KW anti-lipaemic; blood glucose; glucokinase regulatory protein; liver;

Qy	121	CCCTTAAGGAACTGGCAGAGCCCTTCAGGACTATGGTGTGACTCTAGCTTCAGCGTG	180
Db	121	CCCTTAAGGAACTGGCAGAGCCCTTCAGGACTATGGTGTGACTCTAGCTTCAGCGTG	180
Qy	181	CCTCCACCATGGGTGAAGTCTGGGGCAGGCACACGAGCTGGTTGCTAACCTC	240
Db	181	CCTCCACCATGGGTGAAGTCTGGGGCAGGCACACGAGCTGGTTGCTAACCTC	240
Qy	241	GTTAACCTTCCACTGAGCACAGCCAGGTGCGCTGAGATCCAGGGAGAACAGGGC	300
Db	241	GTTAACCTTCCACTGAGCACAGCCAGGTGCGCTGAGATCCAGGGAGAACAGGGC	300
Qy	301	GTCTTCAAGGTTCTTCAGGGCTTACATGGCTGTGCGCGCTGAGGGAGAGATG	420
Db	301	GTCTTCAAGGTTCTTCAGGGCTTACATGGCTGTGCGCGCTGAGGGAGAGATG	420
Qy	361	CGGAATGAGGTTCTTCAGGGCTTACATGGCTGTGCGCGCTGAGGGAGAGATG	420
Db	361	CGGAATGAGGTTCTTCAGGGCTTACATGGCTGTGCGCGCTGAGGGAGAGATG	420
Qy	421	AGCTTGTGCTTCCATCGCAATGGCCCTATGACTCGTCAAGCAGCAGGTGACCCC	480
Db	421	AGCTTGTGCTTCCATCGCAATGGCCCTATGACTCGTCAAGCAGCAGGTGACCCC	480
Qy	481	GGCGGGCAACTCCAGCCCTACTTCCCGATTGGCCACTGACCACAGGACCATG	540
Db	481	GGCGGGCAACTCCAGCCCTACTTCCCGATTGGCCACTGACCACAGGACCATG	540
Qy	541	GGCGTGACTGTGCCAGCCACAGATGTTGGTGAAGGGTCCATTAGGGAGCATAC	600
Db	541	GGCGTGACTGTGCCAGCCACAGATGTTGGTGAAGGGTCCATTAGGGAGCATAC	600
Qy	601	CTCGGGCCATCCAGGAGCAGAAATAACAGCGGACTATAGAACCTACAGAACCATC	660
Db	601	CTCGGGCCATCCAGGAGCAGAAATAACAGCGGACTATAGAACCTACAGAACCATC	660
Qy	661	GGCGGGAGAGGGTCAAGGGCTGGAAAGGAACTTGGCCACATCTGGAAAT	720
Db	661	GGCGGGAGAGGGTCAAGGGCTGGAAAGGAACTTGGCCACATCTGGAAAT	720
Qy	721	GCTATGTCACTGTGCTGAAGGTGACTTACGAGCATCTCAAGGAGGTGCTGAC	780
Db	721	GCTATGTCACTGTGCTGAAGGTGACTTACGAGCATCTCAAGGAGGTGCTGAC	780
Qy	781	TACCCCTCTCACTGACAATCTCCCTGCACTTGTCTGCTCTGCTTGTGAGGCCCTC	840
Db	781	TACCCCTCTCACTGACAATCTCCCTGCACTTGTCTGCTCTGCTTGTGAGGCCCTC	840
Qy	841	TGTGCCCCAGTGGTGGCTCCCGTGGACCTGGTGAAGACCCGGTATAGAACCTC	900
Db	841	TGTGCCCCAGTGGTGGCTCCCGTGGACCTGGTGAAGACCCGGTATAGAACCTC	900
Qy	901	CCAGGCCAGTACTTCAGCCCCCTGCACTGTGATGATAAGATGGTGGCCAGAGGGCCCC	960
Db	901	CCAGGCCAGTACTTCAGCCCCCTGCACTGTGATGATAAGATGGTGGCCAGAGGGCCCC	960
Qy	961	ACACGCTTCAACAGGGATTACACCCCTCT	991
Db	961	ACACGCTTCAACAGGGATTACACCCCTCT	991

Search completed: May 18, 2004, 12:31:25  
Job time : 532 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 17, 2004, 11:50:46 ; Search time 23 Seconds

(without alignments)  
700.318 Million cell updates/sec

Title: US-09-423-410-4  
Perfect score: 1620

Sequence: MVGLKPSDVPPTMVKFGLA.....TYEQLKRALMKVQMLRESSPF 312

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched:  
389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*

2: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*

3: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*

4: /cgn2\_6/ptodata/2/iaa/FCIUS\_COMB.pep:\*

5: /cgn2\_6/ptodata/2/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

\*

Query

Result No. Score Match Length DB ID

Description

RESULT 1  
US-09-142-565-2

; Sequence 2, Application US/09142565A

; Patent No. 618560

; GENERAL INFORMATION:

; APPLICANT: Lee James Beeley

; APPLICANT: Robert James

; TITLE OF INVENTION: NOVEL COMPOUNDS

; FILE REFERENCE: GH-3 002

; CURRENT APPLICATION NUMBER: US/09/142,565A

; CURRENT FILING DATE: 1999-06-30

; EARLIER APPLICATION NUMBER: 9704551.2

; EARLIER FILING DATE: 1997-01-05

; EARLIER APPLICATION NUMBER: 9705614.7

; EARLIER FILING DATE: 1997-01-18

; EARLIER APPLICATION NUMBER: 97305305.1

; EARLIER FILING DATE: 1997-07-16

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 2

; LENGTH: 312

; TYPE: PRT

; ORGANISM: HOMO SAPIEN

US-09-142-565-2

ALIGNMENTS

28	1098	67.8	256	3	US-09-503-579-6	Sequence 6, Appli
29	1012.5	62.5	303	1	US-08-294-522B-36	Sequence 36, Appli
30	1009.5	62.3	303	1	US-08-518-87BB-37	Sequence 37, Appli
31	1009.5	62.3	303	2	US-08-807-661A-37	Sequence 37, Appli
32	1009.5	62.3	303	2	US-08-470-868A-37	Sequence 37, Appli
33	1009.5	62.3	303	3	US-09-210-681-37	Sequence 37, Appli
34	1009.5	62.3	303	3	US-08-946-719A-37	Sequence 37, Appli
35	1009.5	62.3	303	4	US-09-547-983-37	Sequence 37, Appli
36	910.5	56.2	307	4	US-09-743-847-3	Sequence 3, Appli
37	889.5	54.9	307	2	US-08-807-661A-56	Sequence 56, Appli
38	889.5	54.9	307	3	US-09-210-681-56	Sequence 56, Appli
39	889.5	54.9	307	4	US-08-946-719A-56	Sequence 56, Appli
40	889.5	54.9	307	4	US-09-547-983-56	Sequence 1, Appli
41	887	54.8	306	5	PCT-US94-03799-1	Sequence 2, Appli
42	512	31.6	290	4	US-09-433-847-2	Sequence 118, Appli
43	512	31.6	335	4	US-09-482-273-118	Sequence 2, Appli
44	509.5	31.5	291	4	US-09-501-558-2	Sequence 6, Appli
45	485	29.9	95	3	US-09-142-565-6	Sequence 6, Appli

QY 301 LMKVQMLRESPP 312 ; CURRENT FILING DATE: 1999-11-04  
; Sequence 2, Application US/09808457 ; EARLIER APPLICATION NUMBER: PCT/EP98/02645  
Db 301 LMKVQMLRESPP 312 ; EARLIER FILING DATE: 1999-05-05  
; EARLIER APPLICATION NUMBER: 1072/97  
; EARLIER FILING DATE: 1997-05-07  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 312  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Protein UCP3L  
; US-09-423-410-4  
Query Match 100.0%; Score 1620; DB 4; Length 312;  
Best Local Similarity 100.0%; Pred. No. 1.e-179; Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MVGLKPSDVPPTMKAVKFGTACFADLVTPFLDTAKVRQIOTQENQAVQATARLYVQRG 60  
Db 1 MVGLKPSDVPPTMKAVKFGTACFADLVTPFLDTAKVRQIOTQENQAVQATARLYVQRG 60  
QY 61 VLGTTILMVRLTRGEGPSPYNGIVAGLQRQMSFASIRGLYNSVKQVTPKGADNSLITRI 120  
Db 61 VLGTTILMVRLTRGEGPSPYNGIVAGLQRQMSFASIRGLYNSVKQVTPKGADNSLITRI 120  
QY 121 LAGCTGAMAVTCOPTDVKURFOASHLGSRSRDRKRYGTMAYRTIAREEGVGLWK 180  
Db 121 LAGCTGAMAVTCOPTDVKURFOASHLGSRSRDRKRYGTMAYRTIAREEGVGLWK 180  
QY 181 GTLPNIMTAVNCAEVVTIDKEKLDDHLLTONPPCHVSAGAGFCATVVASPVDV 240  
Db 181 GTLPNIMTAVNCAEVVTIDKEKLDDHLLTONPPCHVSAGAGFCATVVASPVDV 240  
QY 241 VKTRYMMSPPGOYFSPLDCMVKMVAQEGPTAFYKGFTPSFLRGLSNVVVMFTYEOULKRA 300  
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QY 301 LMKVQMLRESPP 312  
Db 301 LMKVQMLRESPP 312  
; RESULT 4  
US-09-743-847-5 ; Sequence 5, Application US/09743847  
; General Information:  
; Patent No. 6602694  
; Applicant: Amulyn Pharmaceuticals, Inc.  
; Applicant: Albrand, Keith  
; Applicant: Beaumont, Kevin  
; Applicant: Young, Andrew  
; Title of Invention: UNCOUPLED PROTEIN 4 (UCP-4) AND METHODS OF USE  
; File Reference: 235/108 -0026  
; Current Application Number: US/09/743, 847  
; Current Filing Date: 2001-06-27  
; Prior Application Number: US 60/092, 737  
; Prior Filing Date: 1998-07-14  
; Prior Application Number: PCT/US99/15861  
; Prior Filing Date: 1999-07-14  
; Number of Seq ID Nos: 5  
; Software: Patentin version 3.1  
; Seq ID No 5  
; Length: 310  
; Type: PRT  
; Organism: Homo sapiens  
; US-09-743-847-5  
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Best Local Similarity 99.4%; Pred. No. 3.1e-177; Matches 310; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

RESULT 3  
US-09-423-410-4  
; Sequence 4, Application US/09423410  
; General Information:  
; Patent No. 6620594  
; Applicant: Giacobino, Jean-Paul  
; Applicant: Muzzin, Patrick  
; Applicant: Boss, Olivier  
; Title of Invention: UNCOUPLING PROTEIN HOMOLOGUE: UCP3  
; File Reference: 4-0353/A  
; Current Application Number: US/09/423, 410

QY 1 MNGLKPSDVPTPMAVKELGAGINACFAIDLVTPPLDPAKAVRLQIQLQGENOAVQATRLVOYRG 60  
Db 1 MVGLKPSDVPTPMAVKELGAGINACFAIDLVTPPLDPAKAVRLQIQLQGENOAVQATRLVOYRG 60

QY 61 VLGTLTMRTEGCPSPYNGVLQGLOMSPASIRIGLYDSVKQVTPKGADNSLITRI 120  
Db 61 VLGTLTMRTEGCPSPYNGVLQGLOMSPASIRIGLYDSVKQVTPKGADNSLITRI 120

QY 121 LGCTTGAMAVTCQAOPTDVVKVRQASHIHLGSPRSRDKSGTMDAIRTARBEGRGLWK 180  
Db 121 LGCTTGAMAVTCQAOPTDVVKVRQASHIHLGSPRSRDKSGTMDAIRTARBEGRGLWK 180

QY 181 GTLPNIMRNAIVCAEVYTVDIKEKLDYHLLTDNFPCPCHVSAFGAGFCATVVASPDV 240  
Db 181 GTLPNIMRNAIVCAEVYTVDIKEKLDYHLLTDNFPCPCHVSAFGAGFCATVVASPDV 240

QY 299 LMKVOMLRESPF 310  
Db 299 LMKVOMLRESPF 310

RESULT 5  
US-09-808-457-4  
; Sequence 4, Application US/09808457  
; Patent No. 660038  
; GENERAL INFORMATION:  
; APPLICANT: Boettcher, Brian  
; APPLICANT: Coplan, Shari  
; APPLICANT: Koleko, Michael  
; APPLICANT: Connely, Sheila  
; APPLICANT: Desai, Urvi  
; APPLICANT: Slosberg, Eric  
; TITLE OF INVENTION: Methods and Compositions For Treatment  
; TITLE OF INVENTION: Of Diabetes and Related Conditions via Gene Therapy  
; FILE REFERENCE: 4-31353A/USN  
; CURRENT APPLICATION NUMBER: US/09/808,457  
; CURRENT FILING DATE: 2001-03-14  
; PRIOR APPLICATION NUMBER: 60/XXX,XXX  
; PRIOR FILING DATE: 2000-03-15  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 275  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Protein UCP3S  
; US-09-808-457-4

Query Match 88.3%; Score 1430; DB 4; Length 275;  
Best Local Similarity 100.0%; Pred. No. 1.1e-157; Indels 0; Gaps 0;  
Matches 275; Conservative 0; Mismatches 0; InDel 0;

QY 1 MNGLKPSDVPTPMAVKELGAGINACFAIDLVTPPLDPAKAVRLQIQLQGENOAVQATRLVOYRG 60  
Db 1 MVGLKPSDVPTPMAVKELGAGINACFAIDLVTPPLDPAKAVRLQIQLQGENOAVQATRLVOYRG 60

QY 61 VLGTLTMRTEGCPSPYNGVLQGLOMSPASIRIGLYDSVKQVTPKGADNSLITRI 120  
Db 61 VLGTLTMRTEGCPSPYNGVLQGLOMSPASIRIGLYDSVKQVTPKGADNSLITRI 120

QY 121 LGCTTGAMAVTCQAOPTDVVKVRQASHIHLGSPRSRDKSGTMDAIRTARBEGRGLWK 180  
Db 121 LGCTTGAMAVTCQAOPTDVVKVRQASHIHLGSPRSRDKSGTMDAIRTARBEGRGLWK 180

QY 181 GTLPNIMRNAIVCAEVYTVDIKEKLDYHLLTDNFPCPCHVSAFGAGFCATVVASPDV 240  
Db 181 GTLPNIMRNAIVCAEVYTVDIKEKLDYHLLTDNFPCPCHVSAFGAGFCATVVASPDV 240

QY 241 VKTRYMNSPPGQFTSPUDCMIKWQAQEGPTAFYKG 275  
Db 241 VKTRYMNSPPGQFTSPUDCMIKWQAQEGPTAFYKG 275

RESULT 6  
US-09-423-410-6  
; Sequence 6, Application US/09423410  
; Patent No. 6620594  
; GENERAL INFORMATION:  
; APPLICANT: Glacobino, Jean-Paul  
; APPLICANT: Muzzin, Parrick  
; APPLICANT: Bobis, Olivier  
; TITLE OF INVENTION: UNCOUPLING PROTEIN HOMOLOGUE: UCP3  
; FILE REFERENCE: 4-3033/A  
; CURRENT APPLICATION NUMBER: US/09/423, 410  
; CURRENT FILING DATE: 1999-11-04  
; EARLIER APPLICATION NUMBER: PCT/EP98/02645  
; EARLIER FILING DATE: 1998-05-05  
; EARLIER APPLICATION NUMBER: 1072/97  
; EARLIER FILING DATE: 1997-05-07  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEO\_ID NO 6  
; LENGTH: 275  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Protein UCP3S  
; US-09-423-410-6

Query Match 88.3%; Score 1430; DB 4; Length 275;  
Best Local Similarity 100.0%; Pred. No. 1.1e-157; Indels 0; Gaps 0;  
Matches 275; Conservative 0; Mismatches 0; InDel 0;

QY 1 MNGLKPSDVPTPMAVKELGAGINACFAIDLVTPPLDPAKAVRLQIQLQGENOAVQATRLVOYRG 60  
Db 1 MVGLKPSDVPTPMAVKELGAGINACFAIDLVTPPLDPAKAVRLQIQLQGENOAVQATRLVOYRG 60

QY 61 VLGTLTMRTEGCPSPYNGVLQGLOMSPASIRIGLYDSVKQVTPKGADNSLITRI 120  
Db 61 VLGTLTMRTEGCPSPYNGVLQGLOMSPASIRIGLYDSVKQVTPKGADNSLITRI 120

QY 121 LGCTTGAMAVTCQAOPTDVVKVRQASHIHLGSPRSRDKSGTMDAIRTARBEGRGLWK 180  
Db 121 LGCTTGAMAVTCQAOPTDVVKVRQASHIHLGSPRSRDKSGTMDAIRTARBEGRGLWK 180

QY 181 GTLPNIMRNAIVCAEVYTVDIKEKLDYHLLTDNFPCPCHVSAFGAGFCATVVASPDV 240  
Db 181 GTLPNIMRNAIVCAEVYTVDIKEKLDYHLLTDNFPCPCHVSAFGAGFCATVVASPDV 240

QY 241 VKTRYMNSPPGQFTSPUDCMIKWQAQEGPTAFYKG 275  
Db 241 VKTRYMNSPPGQFTSPUDCMIKWQAQEGPTAFYKG 275

RESULT 7  
US-08-937-466-2  
; Sequence 2, Application US/08937466  
; Patent No. 594679  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Ning  
; APPLICANT: Amaral, M. Catherine  
; APPLICANT: Chen, Jin-Long  
; TITLE OF INVENTION: UCP3 Genes  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSE: SCIENCE & TECHNOLOGY LAW GROUP  
; STREET: 75 DENISE DRIVE  
; CITY: HILLSBOROUGH  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94010

COMPUTER READABLE FORM:  
 COMPUTER TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/937,466  
 FILING DATE:  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: OSMAN, RICHARD A  
 REGISTRATION NUMBER: 36,627  
 REFERENCE/DOCKET NUMBER: T97-009  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650) 343-4341  
 TELEFAX: (650) 343-4341  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 308 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-937-466-2

Query Match 84.5%; Score 1369; DB 2; Length 308;  
 Best Local Similarity 85.3%; Pred. No. 1.7e-150; Matches 266; Conservative 18; Mismatches 24; Indels 4; Gaps 2;

Qy 1 MVGLKPSDVPPTVMAKFLGAGTACFADLIVPLDTAKVRLOQENQAVQTLVYRG 60  
 Db 1 MVGLKPSDVPPTVMAKFLGAGTACFADLIVPLDTAKVRLOQENQAVQTLVYRG 57

Qy 61 VLGILTLMWRTEGPSPNGLVAGLQRMQSFAIRIGLYDSVKQYTPKGADHSVAIRI 120  
 Db 58 VLGILTLMWRTEGPSPNGLVAGLQRMQSFAIRIGLYDSVKQYTPKGADHSVAIRI 117

Qy 121 LAGCTTGAMAVTAQOPTDVVKURFOASLHGLPDRCKSGTMAYRTIAREGVRLWK 180  
 Db 118 LAGCTTGAMAVTAQOPTDVVKURFOAMRLG-TGGERKRYGTMAYRTIAREGVRLWK 176

Qy 181 GTLPNTMNAVCAEVYTIDIKELDYLTDNFCHFVSAFGAGFCATVWASPVDV 240  
 Db 177 GTWPNTITNAIVCAEMTYDIKEKULSHLTDNFCHFVSAFGAGFCATVWASPVDV 236

Qy 241 VKTRYMMSPPGOFSPDLCMVKQVAQSPPTAFYKGFPSFLRIGAWNNMMPVTEQKRA 300  
 Db 237 VKTRYMMAPLGRYRSPDLCMVKQMAQSPPTAFYKGFPSFLRIGAWNNMMPVTEQKRA 296

Qy 301 LMKVQMLRBSPP 312  
 Db 297 LMKVQVLRBSPP 308

RESULT 8  
 US-09-172-528-2  
 Sequence 2, Application US/09172528  
 Patent No. 595469  
 GENERAL INFORMATION:  
 APPLICANT: Zhang, Ning  
 APPLICANT: Amara, M. Catherine  
 APPLICANT: Chen, Jin-Long  
 TITLE OF INVENTION: UCP3 Genes  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
 STREET: 75 DENISE DRIVE  
 CITY: HILLSBOROUGH  
 STATE: CALIFORNIA  
 COUNTRY: USA  
 ZIP: 94010  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk

---

COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/172,528  
 FILING DATE:  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 REFERENCE/DOCKET NUMBER: T97-009  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650) 343-4341  
 TELEFAX: (650) 343-4341  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 308 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-09-172-528-2

Query Match 84.5%; Score 1369; DB 2; Length 308;  
 Best Local Similarity 85.3%; Pred. No. 1.7e-150; Matches 266; Conservative 18; Mismatches 24; Indels 4; Gaps 2;

Qy 1 MVGLKPSDVPPTVMAKFLGAGTACFADLIVPLDTAKVRLOQENQAVQTLVYRG 60  
 Db 1 MVGLKPSDVPPTVMAKFLGAGTACFADLIVPLDTAKVRLOQENQAVQTLVYRG 57

Qy 61 VLGILTLMWRTEGPSPNGLVAGLQRMQSFAIRIGLYDSVKQYTPKGADHSVAIRI 120  
 Db 58 VLGILTLMWRTEGPSPNGLVAGLQRMQSFAIRIGLYDSVKQYTPKGADHSVAIRI 117

Qy 121 LAGCTTGAMAVTAQOPTDVVKURFOASLHGLPDRCKSGTMAYRTIAREGVRLWK 180  
 Db 118 LAGCTTGAMAVTAQOPTDVVKURFOAMRLG-TGGERKRYGTMAYRTIAREGVRLWK 176

Qy 181 GTLPNTMNAVCAEVYTIDIKELDYLTDNFCHFVSAFGAGFCATVWASPVDV 240  
 Db 177 GTWPNTITNAIVCAEMTYDIKEKULSHLTDNFCHFVSAFGAGFCATVWASPVDV 236

Qy 241 VKTRYMMSPPGOFSPDLCMVKQVAQSPPTAFYKGFPSFLRIGAWNNMMPVTEQKRA 300  
 Db 237 VKTRYMMAPLGRYRSPDLCMVKQMAQSPPTAFYKGFPSFLRIGAWNNMMPVTEQKRA 296

Qy 301 LMKVQMLRBSPP 312  
 Db 297 LMKVQVLRBSPP 308

RESULT 9  
 US-09-318-199-2  
 Sequence 2, Application US/09318199  
 Patent No. 603469  
 GENERAL INFORMATION:  
 APPLICANT: Zhang, Ning  
 APPLICANT: Amara, M. Catherine  
 APPLICANT: Chen, Jin-Long  
 TITLE OF INVENTION: UCP3 Genes  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
 STREET: 75 DENISE DRIVE  
 CITY: HILLSBOROUGH  
 STATE: CALIFORNIA  
 COUNTRY: USA  
 ZIP: 94010  
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/318,199  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/937,466  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A.  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-009  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 343-4341  
TELEFAX: (650) 343-4342  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 308 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

MEDICAL COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/503,579  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US/08/937,466  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A.  
REGISTRATION NUMBER: 36,627  
REFERENCE DOCKET NUMBER: T97-009  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 343-4341  
TELEFAX: (650) 343-4342  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 300 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

Best Local Similarity	Score	Matches
85.3%	1	266, Conservative 18; Miami
	1	MVGLKRSDDVPPTMAVEFLGAGTAACPA
	1	MVGLQPSSEVPPTIVKFLGAGTAACPA
	61	VIGTITLMVRTEGGPSVSYNGIVAGIQR
	58	VIGTILTMVRTEGGPSVSYNGIVAGIHR
	121	LAGCTGAGAMAVTCAGTPTDVKVRFOAS
	118	LAGCTGAGAMAVTCAGTPTDVKVRFOAM
	181	GTLPNIRNATUNCAEVNTDILKEKL
	177	GWPNPNTRNAVNCAEVNTDILKEKL
	241	VCTRYNNPSPGOYFSPIDCMKVMVAQE
	301	LMKYQURESPF 312
	237	VKTRYNNPLGKRYSPHLCHMUKMVAQE
	297	LMKVQURESPF 308

RESULT 10

US-09-503-579-2  
Sequence 2, Application US/09503579  
; Patent No. 6248561  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Ning  
; APPLICANT: Amara, M. Catherine  
; TITLE OF INVENTION: UCP3 Genes  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCIENCE & TECHNOLOGY L  
; STREET: 75 DENISE DRIVE  
; CITY: HILLSBOROUGH  
; STATE: CALIFORNIA  
; COUNTRY: USA  
ZIP: 94010

Query Match Score 1369; DB 3; Length 308;  
 Best Local Similarity 85.3%; Pred. No. 1.7e-150; 18: Mismatches  
 Matches 266; Conservative 18; Indels 4; Gaps 2;  
 OY 1 MVGLKPSDVPTMVKWKEFLGAGTAAACFADLUTPFLDTAKVRLQIQQGENQVQARLNQRG 60  
 Db |||||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:  
 1 MVGLQPSSEVPPTVVKELGAGTAAACFADLUTPFLDTAKVRLQIQQGENGAQS--VQRG 57  
 QY 61 VIGCTLTIVWRTEGRCSPNGLVAGLQRMSPASIRIGLYDSVQVYTERKGADNSLTTI 120  
 Db |||||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:  
 58 VIGCTLTIVWRTEGRCSPNGLVAGLQRMSPASIRIGLYDSVQVYTERKGADNSLTTI 117  
 QY 121 LAGCTTGAMAVCAQPTDVKRQFQASIHGSRSDRCGSGMTDAYRTARESGVRGLW 180  
 Db |||||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:  
 118 LAGCTTGAMAVCAQPTDVKRQFQAMRLG-TGGERKXRTGMDAYRTARESGVRGLW 176  
 QY 181 GTLPNIMMNAIVCAEVYTDILKEKLUDYLITDNPFCHFVSAARGFCATVVASPVYD 240  
 Db |||||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:  
 177 GTWPNTTNAIVCAEVYTDILKEKJLESHLTDPNFCHFVSAAGFCATVVASPVYD 236  
 QY 241 VKTRYMMNRPQGQFTSPIDCMIKAVAQEGPTAFYKGFTSFLRIGSVWNVMFTVQLKRA 300  
 Db |||||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:  
 237 VKTRYMMNAPLGRTRSPIDCMIKAVQEGPTAFYKGFTSVLQWVQDQGTA 296  
 QY 301 LMKQWMLRSPP 312  
 Db |||||: :|||: :|||: :|||: :|||:  
 297 LMKQWMLRSPP 308

RESULT 11

US-08-937-466-4

; Sequence 4, Application US/08937466

; Patent No. 5846779

; GENERAL INFORMATION:

; APPLICANT: Zhang, Ning

; APPLICANT: Amaral, M. Catherine

; APPLICANT: Chen, Jin-Long

TITLE OF INVENTION: UCPS Genes

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 75 DENISE DRIVE

CITY: HILLSBOROUGH

STATE: CALIFORNIA

COUNTRY: USA



## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/Ma-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/318,199

FILING DATE:

CLASSIFICATION:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/937,466

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: T77-009

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 343-4341

TELEFAX: (650) 343-4342

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 432 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-318-199-4

Query Match 82.8%; Score 1341; DB 3; Length 432;

Best Local Similarity 85.6%; Pred. No. 5,1e-147; Mismatches 23; Indels 4; Gaps 2;

Matches 261; Conservative 17; Mismatches 23; Indels 4; Gaps 2;

Query 1 MWGLKPSDVPPTMAVKFLGAGTACAFADLVLTPLDATKVRLOIQGENAVAVTARLVQYRG 60

Db 1 MWGLQPSVPPTVVKFLGAGTACAFADLVLTPLDATKVRLOIQGENPGAPS---VQTRG 57

Query 61 VLGTLTILNVRTSPCSPYNGVAGLQRQMSFAIRGIGYDSVQYTKGADNSLLTRI 120

Db 58 VLGTLTILNVRTSPCSPYNGVAGLQRQMSFAIRGIGYDSVQYTKGADHSSVTRI 117

Query 121 LAGCTTGAMAVTCQAOPDVKVRFQASITHLGPERSDRSKYSGTMDAYRTIAREGVGJWK 180

Db 118 LAGCTTGAMAVTCQAOPDVKVRFQASITHLGPERSDRSKYSGTMDAYRTIAREGVGJWK 176

Query 61 VLGTLTILNVRTSPCSPYNGVAGLQRQMSFAIRGIGYDSVQYTKGADNSLLTRI 120

Db 58 VLGTLTILNVRTSPCSPYNGVAGLQRQMSFAIRGIGYDSVQYTKGADHSSVTRI 117

Query 121 LAGCTTGAMAVTCQAOPDVKVRFQASITHLGPERSDRSKYSGTMDAYRTIAREGVGJWK 180

Db 118 LAGCTTGAMAVTCQAOPDVKVRFQAMRLIG-TGGERKRGTMDAYRTIAREGVGJWK 176

Query 181 GTLNIMMNAIVCAEVTYDIKEKLDYHLTDNFPCPHFVSAFGACCATVVASPTDV 240

Db 177 GTWNITNAIVCAEVTYDIKEKLESHLFTDNFPCPHFVSAFGACCATVVASPTDV 236

Query 181 GTLNIMMNAIVCAEVTYDIKEKLDYHLTDNFPCPHFVSAFGACCATVVASPTDV 240

Db 177 GTWNITNAIVCAEVTYDIKEKLESHLFTDNFPCPHFVSAFGACCATVVASPTDV 236

Query 241 VKTRYMNNSPPGQFSPLDMCMKAVAKAQBEGPTAFYKGFFPSFLRGSWNVNMFVTEQLGRA 300

Db 237 VKTRYMNNSPLGRYRSPLCMKAVAKAQBEGPTAFYKGFFPSFLRGSWNVNMFVTEQLGRA 296

Query 301 LMKVQ 305

Db 297 LMKVQ 301

Query 301 LMKVQ 305

Query Match 82.8%; Score 1341; DB 3; Length 432;

Best Local Similarity 85.6%; Pred. No. 5,1e-147; Mismatches 23; Indels 4; Gaps 2;

Matches 261; Conservative 17; Mismatches 23; Indels 4; Gaps 2;

Query 1 MWGLKPSDVPPTMAVKFLGAGTACAFADLVLTPLDATKVRLOIQGENAVAVTARLVQYRG 60

Db 1 MWGLQPSVPPTVVKFLGAGTACAFADLVLTPLDATKVRLOIQGENPGAPS---VQTRG 57

Query 61 VLGTLTILNVRTSPCSPYNGVAGLQRQMSFAIRGIGYDSVQYTKGADNSLLTRI 120

Db 58 VLGTLTILNVRTSPCSPYNGVAGLQRQMSFAIRGIGYDSVQYTKGADHSSVTRI 117

Query 121 LAGCTTGAMAVTCQAOPDVKVRFQASITHLGPERSDRSKYSGTMDAYRTIAREGVGJWK 180

Db 118 LAGCTTGAMAVTCQAOPDVKVRFQAMRLIG-TGGERKRGTMDAYRTIAREGVGJWK 176

Query 181 GTLNIMMNAIVCAEVTYDIKEKLDYHLTDNFPCPHFVSAFGACCATVVASPTDV 240

Db 177 GTWNITNAIVCAEVTYDIKEKLESHLFTDNFPCPHFVSAFGACCATVVASPTDV 236

Query 181 GTLNIMMNAIVCAEVTYDIKEKLDYHLTDNFPCPHFVSAFGACCATVVASPTDV 240

Db 177 GTWNITNAIVCAEVTYDIKEKLESHLFTDNFPCPHFVSAFGACCATVVASPTDV 236

Query 241 VKTRYMNNSPPGQFSPLDMCMKAVAKAQBEGPTAFYKGFFPSFLRGSWNVNMFVTEQLGRA 300

Db 237 VKTRYMNNSPLGRYRSPLCMKAVAKAQBEGPTAFYKGFFPSFLRGSWNVNMFVTEQLGRA 296

Query 301 LMKVQ 305

Db 297 LMKVQ 301

## ZIP: 94010

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/503,579

FILING DATE:

CLASSIFICATION:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US/08/937,466

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: T77-009

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 343-4341

TELEFAX: (650) 343-4342

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 432 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-503-579-4

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/503,579

FILING DATE:

CLASSIFICATION:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US/08/937,466

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: T77-009

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 343-4341

TELEFAX: (650) 343-4342

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 432 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-503-579-4

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/503,579

FILING DATE:

CLASSIFICATION:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US/08/937,466

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: T77-009

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 343-4341

TELEFAX: (650) 343-4342

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 432 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-503-579-4

CURRENT APPLICATION NUMBER: US/10/001,051B  
CURRENT FILING DATE: 2002-06-25  
PRIOR APPLICATION NUMBER: US 60/244,946  
PRIOR FILING DATE: 2000-11-01  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 2  
LENGTH: 309  
TYPE: PRT  
ORGANISM: Unknown Organism  
FEATURE:  
OTHER INFORMATION: Description of Unknown Organism: Any animal  
US-10-001-051B-2  
OTHER INFORMATION: source, typically mammalian, most typically human

Query Match 71.1%; Score 1152.5; DB 4; Length 309;  
Best Local Similarity 72.2%; Pred. No. 2.5e-125; Mismatches 50; Indels 5; Gaps 3;  
Matches 226; Conservative 32; Mismatches 50; Indels 5; Gaps 3;  
QY 1 MVLKSDVPTMAVKELGASTACADLVTPLDTAKVRLIQIGENOA-VOTARLUQVR 59  
Db 1 MVGKATDVPPTATVKELGAFPACTADLITPLDTAKVRLIQGSQGPVATASAQYR 60  
QY 60 GVLTGILMVRTEGPGSPYNSIVAGLQRQMAPASITIGLIVSVQVQTPKAHDNLTR 119  
Db 61 GWMGTGILMVRTEGPGSPYNSIVAGLQRQMAPASVRIGLIVSVQVQTPKAHDNLTR 119  
QY 120 ILAGCTTGAMAVTCAPTDVVKVRFOSIHSIIGPSRSRDRKVGTMDAYTIRABEGVGLW 179  
Db 120 ILAGSTTGALLAVAVAOPIDVVKVRFOQARAG---GARRYUSTVNVIKILARBEGVGLW 176  
QY 180 KOTLPINMRNLAUNCAEVUTDILKEKLDYHILTONPCIFVSARGAGRAVTVASPVD 239  
Db 177 KOTSPNVTARNATVNCALIVTYPOLIKOALKANIWTDDLPCHIPSARGAGFCUTVIASPVD 236  
QY 240 VIKTRIMSPFGQFSPIDCMKVAQAGPFAFYKGSTPSFLRGSHMVVUTVYQKLK 299  
Db 237 VIKTRIVNSALQYSSAGCHALTMQREGPRAFYKGMPSTFLRGSHMVVUTVYQKLK 296  
QY 300 ALMKVQMLRESPF 312  
Db 297 ALMAGCTSREAPP 309

Search completed: May 17, 2004, 11:54:30  
Job time : 24 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

### OM protein - protein search, using sw model

Run on: May 17, 2004, 11:53:27 ; Search time 48 Seconds  
(without alignments)  
1808.699 Million cell updates/sec

Title: US-09-423-410-4

Perfect score: 1620

Sequence: MVGLKPSPDVPTMAVKFLGA.....TYEQLKRALMKVQMLRESPP 312

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.\*

1: /cgn2\_6/ptodata/2/pubpaa/us07\_pubcomb.pep:\*

2: /cgn2\_6/ptodata/2/pubpaa/pcpt\_new\_pub.pep:\*

3: /cgn2\_6/ptodata/2/pubpaa/us06\_pub comb.pep:\*

4: /cgn2\_6/ptodata/2/pubpaa/us06\_pubcomb.pep:\*

5: /cgn2\_6/ptodata/2/pubpaa/us07\_new\_pub.pep:\*

6: /cgn2\_6/ptodata/2/pubpaa/pcrtus\_pubcomb.pep:\*

7: /cgn2\_6/ptodata/2/pubpaa/us08\_pubcomb.pep:\*

8: /cgn2\_6/ptodata/2/pubpaa/us08\_pubcomb.pep:\*

9: /cgn2\_6/ptodata/2/pubpaa/us09\_pubcomb.pep:\*

10: /cgn2\_6/ptodata/2/pubpaa/us09\_pubcomb.pep:\*

11: /cgn2\_6/ptodata/2/pubpaa/us09\_pubcomb.pep:\*

12: /cgn2\_6/ptodata/2/pubpaa/us09\_pubcomb.pep:\*

13: /cgn2\_6/ptodata/2/pubpaa/us10\_pubcomb.pep:\*

14: /cgn2\_6/ptodata/2/pubpaa/us10\_pubcomb.pep:\*

15: /cgn2\_6/ptodata/2/pubpaa/us10\_pubcomb.pep:\*

16: /cgn2\_6/ptodata/2/pubpaa/us60\_new\_pub.pep:\*

17: /cgn2\_6/ptodata/2/pubpaa/us60\_pubcomb.pep:\*

18: /cgn2\_6/ptodata/2/pubpaa/us60\_pubcomb.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Query Score Match Length DB ID Description

No. No.

1 1620 100.0 312 9 US-09-734-134-2 Sequence 2, Appli

2 1620 100.0 312 9 US-09-826-507-2 Sequence 2, Appli

3 1620 100.0 312 9 US-09-808-557-2 Sequence 2, Appli

4 1620 100.0 312 12 US-10-671-628-9 Sequence 9, Appli

5 1556 96.0 300 14 US-10-270-861-35 Sequence 35, Appli

6 1430 88.3 275 9 US-09-808-457-4 Sequence 4, Appli

7 1430 88.3 284 10 US-09-823-886A-6 Sequence 6, Appli

8 1152.5 71.1 309 9 US-09-884-814-8 Sequence 8, Appli

9 1152.5 71.1 309 13 US-10-001-051B-2 Sequence 2, Appli

10 1152.5 71.1 309 15 US-10-197-019-3 Sequence 3, Appli

11 1149.5 71.0 309 9 US-09-884-814-1 Sequence 1, Appli

12 1149.5 71.0 309 12 US-10-336-472-132 Sequence 132, Appli

13 1149.5 71.0 309 14 US-10-270-861-34 Sequence 8, Appli

14 1149.5 71.0 309 14 US-10-265-689-1 Sequence 34, Appli

15 1149.5 71.0 309 14 US-10-265-689-1 Sequence 1, Appli

16 1149.5 71.0 314 10 US-09-823-886A-4 Sequence 4, Appli

17 1147.5 70.8 309 9 US-09-884-814-6 Sequence 6, Appli

18 1142.5 70.7 321 12 US-10-472-130 Sequence 130, Appli

19 919 56.7 306 12 US-10-037-417-89 Sequence 89, Appli

20 910.5 56.2 307 10 US-09-823-886A-2 Sequence 2, Appli

21 910.5 56.2 307 12 US-10-037-417-87 Sequence 87, Appli

22 905 55.9 306 12 US-10-037-417-90 Sequence 90, Appli

23 902.5 55.7 307 12 US-10-037-417-88 Sequence 88, Appli

24 902.5 55.7 307 14 US-10-671-628-7 Sequence 7, Appli

25 902.5 55.7 307 12 US-10-270-861-33 Sequence 33, Appli

26 873.5 53.9 307 12 US-10-037-417-91 Sequence 91, Appli

27 736.5 45.5 271 12 US-10-037-417-25 Sequence 26, Appli

28 687 42.4 306 12 US-10-671-628-5 Sequence 5, Appli

29 681.5 42.1 345 12 US-10-425-114-633-7 Sequence 66317, A

30 676 41.7 303 12 US-10-425-114-633-7 Sequence 237636,

31 675.5 41.7 303 12 US-10-671-628-2 Sequence 1, Appli

32 651 40.2 314 12 US-10-671-628-6 Sequence 2, Appli

33 592 36.5 328 14 US-10-671-628-4 Sequence 6, Appli

34 521 32.2 322 14 US-10-270-861-11 Sequence 4, Appli

35 521 32.2 325 14 US-10-270-861-13 Sequence 11, Appli

36 512 31.6 325 14 US-10-270-861-7 Sequence 13, Appli

37 512 31.6 325 14 US-10-270-861-1 Sequence 7, Appli

38 512 31.6 335 10 US-09-984-271-118 Sequence 1, Appli

39 512 31.6 335 12 US-09-984-276-118 Sequence 118, App

40 509 31.4 325 12 US-10-262-551-152 Sequence 152, App

41 500.5 30.9 291 15 US-10-108-60A-247-6 Sequence 2476, AP

42 496.5 30.6 317 12 US-10-424-599-276094 Sequence 276094,

43 496.5 30.1 317 12 US-10-424-599-276095 Sequence 276095,

44 487.5 30.1 341 12 US-10-425-114-52234 Sequence 52234, A

45 486.5 30.0 353 14 US-10-270-861-9 Sequence 9, Appli

### ALIGNMENTS

RESULT 1  
US-09-734-134-2  
Sequence 2, Application US/09734134

PATENT NO. US20100109291

CURRENT APPLICATION NUMBER: US/09734,134

PRIOR APPLICATION NUMBER: GB 970551.2

PRIOR FILING DATE: 1997-03-05

PRIOR APPLICATION NUMBER: GB 9705614.7

PRIOR FILING DATE: 1997-03-18

PRIOR APPLICATION NUMBER: EP 97305305.1

PRIOR FILING DATE: 1997-07-16

PRIOR APPLICATION NUMBER: GB 9800633

PRIOR FILING DATE: 1998-03-02

PRIOR APPLICATION NUMBER: 09142,565

PRIOR FILING DATE: 1999-06-30

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO. 2

LENGTH: 312

TYPE: PRT

ORGANISM: HOMO SAPIENS

Query Match Similarity 100.0%; Score 1620; DB 9; Length 312;

Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-734-134-2

Sequence 4, Appli

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Sequence 8, Appli

Sequence 10, Appli

Sequence 12, Appli

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Sequence 226, Appli

Sequence 228, Appli

Sequence 230, Appli

Sequence 232, Appli

Sequence 234, Appli

Sequence 236, Appli

Sequence 238, Appli

QY 61 VIGTILITMVRTEGCPSPYNGLVAGLQRQMSFASIRIGLYDSVQVTPKGADNSLTTRI 120  
 Db 61 VIGTILITMVRTEGCPSPYNGLVAGLQRQMSFASIRIGLYDSVQVTPKGADNSLTTRI 120  
 QY 121 LAGCTTGAMAVTCQAQPDTDVKVRQFQASIHGLGSRSDRKYSGTMDAYRTIABEGVGLWK 180  
 Db 121 LAGCTTGAMAVTCQAQPDTDVKVRQFQASIHGLGSRSDRKYSGTMDAYRTIABEGVGLWK 180  
 QY 181 GTPLNINRNATNCVAEVTVYDILKEKLDYHLLTDNPFCHVSAFGFCATVVASPVDV 240  
 Db 181 GTPLNINRNATNCVAEVTVYDILKEKLDYHLLTDNPFCHVSAFGFCATVVASPVDV 240  
 QY 241 VCTRYMNSPPGQYFSPLDCMIVKVAQEGPTAFYKGFTPSFLRGSNWVMFVYEQIKRA 300  
 Db 241 VCTRYMNSPPGQYFSPLDCMIVKVAQEGPTAFYKGFTPSFLRGSNWVMFVYEQIKRA 300  
 QY 301 LMKVQMURESPP 312  
 Db 301 LMKVQMURESPP 312

RESULT 2  
 US-09-826-507-2  
 ; Sequence 2, Application US/09826507  
 ; Patent No. US2000004492A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lee James Beeley  
 ; APPLICANT: John Christopher Clapham  
 ; APPLICANT: Robert James Godden  
 ; TITLE OF INVENTION: NEW USE  
 ; FILE REFERENCE: GH-3-009-C1  
 ; CURRENT APPLICATION NUMBER: US/09/826, 507  
 ; CURRENT FILING DATE: 2001-04-05  
 ; PRIOR APPLICATION NUMBER: 09/312, 620  
 ; PRIOR FILING DATE: 1999-05-17  
 ; PRIOR APPLICATION NUMBER: 9814926-3  
 ; PRIOR FILING DATE: 1998-07-09  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO: 2  
 ; LENGTH: 312  
 ; TYPE: PRT  
 ; ORGANISM: Unknown  
 ; FEATURE:  
 ; OTHER INFORMATION: Protein UCP3L

US-09-808-457-2  
 ; Query Match 100.0%; Score 1620; DB 9; Length 312;  
 ; Best Local Similarity 100.0%; Pred. No. 2.2e-167;  
 ; Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 ; Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVGLKSDVPPMAVKLGACTAACADLWVPLDTAKVRUQIQGENAQAVOTARLYQYRG 60  
 Db 1 MVGLKSDVPPMAVKLGACTAACADLWVPLDTAKVRUQIQGENAQAVOTARLYQYRG 60  
 QY 61 VIGTILITMVRTEGCPSPYNGLVAGLQRQMSFASIRIGLYDSVQVTPKGADNSLTTRI 120  
 Db 61 VIGTILITMVRTEGCPSPYNGLVAGLQRQMSFASIRIGLYDSVQVTPKGADNSLTTRI 120  
 QY 121 LAGCTTGAMAVTCQAQPDTDVKVRQFQASIHGLGSRSDRKYSGTMDAYRTIABEGVGLWK 180  
 Db 121 LAGCTTGAMAVTCQAQPDTDVKVRQFQASIHGLGSRSDRKYSGTMDAYRTIABEGVGLWK 180  
 QY 181 GTPLNINRNATNCVAEVTVYDILKEKLDYHLLTDNPFCHVSAFGFCATVVASPVDV 240  
 Db 181 GTPLNINRNATNCVAEVTVYDILKEKLDYHLLTDNPFCHVSAFGFCATVVASPVDV 240  
 QY 241 VCTRYMNSPPGQYFSPLDCMIVKVAQEGPTAFYKGFTPSFLRGSNWVMFVYEQIKRA 300  
 Db 241 VCTRYMNSPPGQYFSPLDCMIVKVAQEGPTAFYKGFTPSFLRGSNWVMFVYEQIKRA 300  
 QY 301 LMKVQMURESPP 312  
 Db 301 LMKVQMURESPP 312

RESULT 3  
 US-09-808-457-2  
 ; Sequence 2, Application US/09808457  
 ; Patent No. US20020065239A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Boettcher, Brian  
 ; APPLICANT: Caplan, Shari  
 ; APPLICANT: Kaleko, Michael  
 ; APPLICANT: Connally, Sheila  
 ; APPLICANT: Desai, Urvi  
 ; APPLICANT: Sloberg, Eric  
 ; TITLE OF INVENTION: Methods and Compositions For Treatment of Diabetes and Related Conditions Via Gene Therapy  
 ; FILE REFERENCE: 4-3153A/USN  
 ; CURRENT APPLICATION NUMBER: US/09/808, 457  
 ; CURRENT FILING DATE: 2001-03-14  
 ; PRIOR APPLICATION NUMBER: 60/XXXX, XXX  
 ; PRIOR FILING DATE: 2000-03-15  
 ; NUMBER OF SEQ ID NOS: 10  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 2  
 ; LENGTH: 312  
 ; TYPE: PRT  
 ; ORGANISM: Unknown  
 ; FEATURE:  
 ; OTHER INFORMATION: Protein UCP3L

US-09-826-507-2  
 ; Query Match 100.0%; Score 1620; DB 9; Length 312;  
 ; Best Local Similarity 100.0%; Pred. No. 2.2e-167;  
 ; Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 ; Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVGLKSDVPPMAVKLGACTAACADLWVPLDTAKVRUQIQGENAQAVOTARLYQYRG 60  
 Db 1 MVGLKSDVPPMAVKLGACTAACADLWVPLDTAKVRUQIQGENAQAVOTARLYQYRG 60  
 QY 61 VIGTILITMVRTEGCPSPYNGLVAGLQRQMSFASIRIGLYDSVQVTPKGADNSLTTRI 120  
 Db 61 VIGTILITMVRTEGCPSPYNGLVAGLQRQMSFASIRIGLYDSVQVTPKGADNSLTTRI 120  
 QY 121 LAGCTTGAMAVTCQAQPDTDVKVRQFQASIHGLGSRSDRKYSGTMDAYRTIABEGVGLWK 180  
 Db 121 LAGCTTGAMAVTCQAQPDTDVKVRQFQASIHGLGSRSDRKYSGTMDAYRTIABEGVGLWK 180  
 QY 181 GTPLNINRNATNCVAEVTVYDILKEKLDYHLLTDNPFCHVSAFGFCATVVASPVDV 240  
 Db 181 GTPLNINRNATNCVAEVTVYDILKEKLDYHLLTDNPFCHVSAFGFCATVVASPVDV 240  
 QY 241 VCTRYMNSPPGQYFSPLDCMIVKVAQEGPTAFYKGFTPSFLRGSNWVMFVYEQIKRA 300  
 Db 241 VCTRYMNSPPGQYFSPLDCMIVKVAQEGPTAFYKGFTPSFLRGSNWVMFVYEQIKRA 300  
 QY 301 LMKVQMURESPP 312  
 Db 301 LMKVQMURESPP 312

RESULT 4  
 US-10-671-628-9  
 ; Sequence 9, Application US/10671628  
 ; Publication No. US20040068105A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ITO, Kikukatsu  
 ; TITLE OF INVENTION: Plant Thermogenic Genes and Proteins  
 ; FILE REFERENCE: 2003-1286A/WMC/00653  
 ; CURRENT APPLICATION NUMBER: US/10/671, 628  
 ; PRIOR APPLICATION NUMBER: 10/009, 962  
 ; PRIOR FILING DATE: 2003-09-29  
 ; PRIOR APPLICATION NUMBER: PCT/JP00/03806  
 ; PRIOR FILING DATE: 2000-06-12  
 ; PRIOR APPLICATION NUMBER: JP11-167439

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; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-671-628-9

Query Match 100.0%; Score 1620; DB 12; length 312;
Best Local Similarity 100.0%; Pred. No. 2.2e-167;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 MVGLKPSDVPPTMAVKFLGAGTACACPAIDLVTPLDTAKVRLQIQLGENAQVQARLVQRG 60
Db 1 MVGLKPSDVPPTMAVKFLGAGTACACPAIDLVTPLDTAKVRLQIQLGENAQVQARLVQRG 60
QY 61 VLGTLTMWTRTEGCSPPNGVLVAGLQIQLGENAQVQARLVQRG 60
QY 61 VLGTLTMWTRTEGCSPPNGVLVAGLQIQLGENAQVQARLVQRG 60
Db 121 LAGCTTGAMAVTCQOPTDVKVRFOASHLGSPRSDRKYSGTMDAYRTIAREGVRLWKGTLPNIMRNIAV 180
Db 121 LAGCTTGAMAVTCQOPTDVKVRFOASHLGSPRSDRKYSGTMDAYRTIAREGVRLWKGTLPNIMRNIAV 180
QY 181 GTLNIMMRMVAIVNCAEVVTDILKEKLDYHLLTDNPFCHPVSARGFCATVVASPVDV 240
QY 181 GTLNIMMRMVAIVNCAEVVTDILKEKLDYHLLTDNPFCHPVSARGFCATVVASPVDV 240
Db 181 GTLNIMMRMVAIVNCAEVVTDILKEKLDYHLLTDNPFCHPVSARGFCATVVASPVDV 240
Db 241 VKTYYMNNSPGQFSPLODCMKVMAQEGTAFAVYKOPTSFLRGSWNVNVMVTVTEQLKRA 300
Db 241 VKTYYMNNSPGQFSPLODCMKVMAQEGTAFAVYKOPTSFLRGSWNVNVMVTVTEQLKRA 300
QY 3.01 LMKVOMLRESPF 312
QY 3.01 LMKVOMLRESPF 312
Db 301 LMKVOMLRESPF 312

RESULT 5
US-10-270-861-35
; Sequence 35, Application US/10270861
; Publication No. US20030077749A1
; GENERAL INFORMATION:
; APPLICANT: Adams, Sean
; APPLICANT: Pan, James
; TITLE OF INVENTION: UCP5
; FILE REFERENCE: P1663R2
; CURRENT APPLICATION NUMBER: US/10/270,861
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US/09/433,622
; PRIOR FILING DATE: 1999-11-02
; PRIOR APPLICATION NUMBER: US 60/110,286
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/129,583
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: US 60/143,886
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 35
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-270-861-35

Query Match 95.0%; Score 1556; DB 14; Length 300;
Best Local Similarity 100.0%; Pred. No. 1.9e-160;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 MAVKFLGAGTACACPAIDLVTPLDTAKVRLQIQLGENAQVQARLVQRGTLTMWTRTE 72
QY 1 MAVKFLGAGTACACPAIDLVTPLDTAKVRLQIQLGENAQVQARLVQRGTLTMWTRTE 60
QY 73 GPCSPYNGLVLVAGLQIQLGENAQVQARLVQRGTLTMWTRTE 132

RESULT 6
US-09-808-457-4
; Sequence 4, Application US/090808457
; Patent No. US20020055239A1
; GENERAL INFORMATION:
; APPLICANT: Boettcher, Brian
; APPLICANT: Caplan, Shari
; APPLICANT: Kaleko, Michael
; APPLICANT: Connely, Sheila
; APPLICANT: Deasi, Urvi
; APPLICANT: Slobberg, Eric
; TITLE OF INVENTION: Methods and Compositions For Treatment of Diabetes and Related Conditions Via Gene Therapy
; FILE REFERENCE: 4-1135A/USN
; CURRENT APPLICATION NUMBER: US/09/808,457
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/XXX,XXX
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE: OTHER INFORMATION: Protein UCP3S
; US-09-808-457-4

Query Match 88.3%; Score 1430; DB 9; Length 275;
Best Local Similarity 100.0%; Pred. No. 8.7e-147;
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVGLKPSDVPPTMAVKFLGAGTACACPAIDLVTPLDTAKVRLQIQLGENAQVQARLVQRG 60
Db 1 MVGLKPSDVPPTMAVKFLGAGTACACPAIDLVTPLDTAKVRLQIQLGENAQVQARLVQRG 60
Db 121 LAGCTTGAMAVTCQOPTDVKVRFOASHLGSPRSDRKYSGTMDAYRTIAREGVRLWKGTLPNIMRNIAV 180
Db 121 LAGCTTGAMAVTCQOPTDVKVRFOASHLGSPRSDRKYSGTMDAYRTIAREGVRLWKGTLPNIMRNIAV 180
QY 181 GTLNIMMRMVAIVNCAEVVTDILKEKLDYHLLTDNPFCHPVSARGFCATVVASPVDV 240
QY 181 GTLNIMMRMVAIVNCAEVVTDILKEKLDYHLLTDNPFCHPVSARGFCATVVASPVDV 240
Db 181 VLGTLTMWTRTEGCSPPNGVLVAGLQIQLGENAQVQARLVQRG 60
Db 241 VKTYYMNNSPGQFSPLODCMKVMAQEGTAFAVYKOPTSFLRGSWNVNVMVTVTEQLKRA 275
Db 241 VKTYYMNNSPGQFSPLODCMKVMAQEGTAFAVYKOPTSFLRGSWNVNVMVTVTEQLKRA 275

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RESULT 7

US-09-823-886A-6

Sequence 6, Application US/09023886A

; Publication No. US20030150022A1

; GENERAL INFORMATION:  
; APPLICANT: Newell, Martha  
; APPLICANT: Betty-Lou, Sandra  
; TITLE OF INVENTION: Compositions and methods for regulating metabolism in plants  
; FILE REFERENCE: C1102/7002  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: US 60/193, 533  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO: 6  
; LENGTH: 284  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-823-886A-6

Query Match 88.3%; Score 1430; DB 10; Length 284;  
Best Local Similarity 100.0%; Pred. No. 9.1e-147; Mismatches 0; Indels 0; Gaps 0;  
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVGLKPSDVPTMAVKFLGAGTACACADLTFPLDTAKVRLQIOPENQA-VOTARLWQRG 60  
Db 10 MVGLKPSDVPTMAVKFLGAGTACACADLTFPLDTAKVRLQIOPENQA-VOTARLWQRG 69

Qy 61 VLGTTLMVRTEGCPSPYNGIVAGLQRQMSAFASIRIGLYDVSQVYTPKGADNSLITR 120  
Db 70 VLGTTLMVRTEGCPSPYNGIVAGLQRQMSAFASIRIGLYDVSQVYTPKGADNSLITR 129

Qy 121 ILAGCTTGAMAVTCACOPTDVKYRFQSHIHLGSPSRKYSCTMDARTIAREBEGRLWK 180  
Db 130 ILAGCTTGAMAVTCACOPTDVKYRFQSHIHLGSPSRKYSCTMDARTIAREBEGRLWK 189

Qy 181 GTLPNIMRNIAVCAEVVTVILKEKLDDYHLLTDPRCHVSARGAGFCITVAVSPDV 240  
Db 190 GTLPNIMRNIAVCAEVVTVILKEKLDDYHLLTDPRCHVSARGAGFCITVAVSPDV 249

Qy 241 VKTRYIMNSPPGQYFSPIDCMTRKNAQBGPTAFYKG 275  
Db 250 VKTRYIMNSPPGQYFSPIDCMTRKNAQBGPTAFYKG 284

RESULT 8  
US-09-884-814-8

; Sequence 8, Application US/0988414  
; Patent No. US2002012760A1  
; GENERAL INFORMATION:  
; APPLICANT: Gonzalez-Zulueta, Mirella  
; APPLICANT: McFarland, K.C.  
; APPLICANT: Chin, Daniel  
; APPLICANT: Shamloo, Mehrdad  
; APPLICANT: Wieloch, Tadeusz  
; APPLICANT: Melcher, Thornton  
; APPLICANT: AGY Therapeutics, Inc.  
; TITLE OF INVENTION: METHODS OF DIAGNOsing, PREVENTING AND TREATING  
; FILE REFERENCE: 01948-003010US  
; CURRENT APPLICATION NUMBER: US10/001, 051B  
; CURRENT FILING DATE: 2002-06-25  
; PRIOR APPLICATION NUMBER: US 60/244, 946  
; PRIOR FILING DATE: 2000-11-01  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO: 2  
; LENGTH: 309  
; TYPE: PRT  
; ORGANISM: Unknown Organism

; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Any animal  
; OTHER INFORMATION: source, typically mammalian, most typically human

US-10-001-051B-2

Query Match 71.1%; Score 1152.5; DB 13; Length 309;  
Best Local Similarity 72.2%; Pred. No. 1.6e-116; Mismatches 5; Indels 5; Gaps 3;  
Matches 226; Conservative 32; Mismatches 5; Indels 5; Gaps 3;

Qy 1 MVGLKPSDVPTMAVKFLGAGTACACADLTFPLDTAKVRLQIOPENQA-VOTARLWQRG 59  
Db 1 MGFKKIDVPTMAVKFLGAGTACACADLTFPLDTAKVRLQIOPENQA-VOTARLWQRG 60

Qy 60 GTLPNIMRNIAVCAEVVTVILKEKLDDYHLLTDPRCHVSARGAGFCITVAVSPDV 119  
Db 61 GVMTTLMVRTEGCPSPYNGIVAGLQRQMSAFASIRIGLYDVSQVYTPKGADNSLITR 119

Qy 120 ILAGCTTGAMAVTCACOPTDVKYRFQSHIHLGSPSRKYSCTMDARTIAREBEGRLWK 179  
Db 120 ILAGSTTGALAVAVAGPTDVKYRFQSHIHLGSPSRKYSCTMDARTIAREBEGRLWK 176

Qy 180 GTLPNIMRNIAVCAEVVTVILKEKLDDYHLLTDPRCHVSARGAGFCITVAVSPDV 239  
Db 177 KGTSPNMRNIAVCAEVVTVILKEKLDDYHLLTDPRCHVSARGAGFCITVAVSPDV 236

RESULT 10  
US-10-197-019-3  
; Sequence 3, Application US/10197019  
; Publication No. US2003020784A1  
; GENERAL INFORMATION:  
; APPLICANT: Chew, Anne  
; APPLICANT: Denton, R. Rex  
; APPLICANT: Gilson, Christopher Raleigh  
; APPLICANT: Nandabalan, Krishnan  
; APPLICANT: Parks, Katie E.  
; TITLE OF INVENTION: HAPLOTYPES OF THE UCP2 GENE  
; FILE REFERENCE: MWH-0042US  
; CURRENT APPLICATION NUMBER: US/10/197,019  
; CURRENT FILING DATE: 2002-07-16  
; PRIOR APPLICATION NUMBER: PCT/US01/02485  
; PRIOR FILING DATE: 2001-01-25  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: PatentIn version 3.1  
; LENGTH: 309  
; SEQ ID NO: 3  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-197-019-3

Query Match 71.1%; Score 1152.5; DB 15; Length 309;  
Best Local Similarity 72.2%; Pred. No. 1.5e-116; Matches 226; Conservative 32; Mismatches 50; Indels 5; Gaps 3; Length: 309

Matches 226; Conservative 31; Mismatches 51; Indels 5; Gaps 3;

Qy 1 MVGLKSDVPPMVKELGAGTACFADLVTPLDTPAKVRLQIQGENQA-VQTARIVQYR 59  
1 MVGPKATDVPTTAKVRLQIQGENQA-VQTARIVQYR 60

Db 60 GVLTGILTMVRTEGCPSPYNGVJAGLQRQMSAFASIRGLDVSQVTPKGADNSLITR 119  
61 GVWTGILTMVRTEGEPISLYNGVJAGLQRQMSAFASIRGLDVSQVTPKGADNSLITR 119

Qy 120 ILAGCTGAMAVTCQOPTDVKURFOASIHGPSRSDRKSYGTMDAYRTIAREEGVGLW 179  
120 ILAGSTGALAVAVAQOPTDVKURFOQARAG--GGRRYQSTVNAKYIARREGGFRGLW 176

Db 120 ILAGSTGALAVAVAQOPTDVKURFOQARAG--GGRRYQSTVNAKYIARREGGFRGLW 176

Qy 180 KGTLPNIMRNALVNCAEVWTDILKEKUDYHLLDNFPCFHSVAGAGRCATVWASPVD 239  
177 KGTSPTVARNALVNCAEVWTDILKEKUDYHLLDNFPCFHSVAGAGRCATVWASPVD 236

Db 240 VVKTRYNNSPGQYFSPLDCMKVMAQEGLPFTPSFLRGLGSNNVMVNTYQQLR 299  
237 VVKTRYNNSAQGQSSAGHCAITMLQEGPRFYKGFMPSFLRGLGSNNVMVNTYQQLR 296

Qy 300 ALMKVQMLRESPF 312  
297 ALMAACTSREAPP 309

Db

RESULT 11  
US-09-884-814-1  
; Sequence 1, Application US/09884814  
; Publication No. US20040043929A1  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, David W.  
; APPLICANT: Ballinger, Robert A.  
; APPLICANT: Baumgartner, Jason C.  
; APPLICANT: Burges, Catherine E.  
; APPLICANT: Casman, Stacie J.  
; APPLICANT: Chant, John S.  
; APPLICANT: Berghs, Constance  
; APPLICANT: Gangolli, Baha A.  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Furtak, Katarzyna  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Gilbert, Jennifer A.  
; APPLICANT: Gunther, Erik  
; APPLICANT: Gorman, Linda  
; APPLICANT: Guo, Xiaoja Sasha  
; APPLICANT: Ji, Weizhen  
; APPLICANT: Li, Li  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Rastelli, Luca  
; APPLICANT: MacDougal, John R.

APPLICANT: Mishra, Vishnu  
 APPLICANT: Pena, Carol E.A.  
 APPLICANT: Spaderina, Steven K.  
 APPLICANT: Shimkets, Richard A.  
 APPLICANT: Spytek, Kimberly A.  
 APPLICANT: Stone, David J.  
 APPLICANT: Shenvoy, Suresh G.  
 APPLICANT: Ort, Tatiana  
 APPLICANT: Tchauder Jr., Raymond J.  
 APPLICANT: Vernet, Corine A.M.  
 APPLICANT: Wolenc, Adam R.  
 APPLICANT: Zerhusen, Bryan D.  
 APPLICANT: Zhong, Mei

TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
 FILE REFERENCE: 21402533C  
 CURRENT APPLICATION NUMBER: US/10/336,472  
 CURRENT FILING DATE: 2003-01-03  
 PRIOR APPLICATION NUMBER: 09/746,491  
 PRIOR FILING DATE: 2000-12-20  
 PRIOR APPLICATION NUMBER: 10/005,041  
 PRIOR FILING DATE: 2001-12-04  
 PRIOR APPLICATION NUMBER: 10/023,681  
 PRIOR FILING DATE: 2001-12-18  
 PRIOR FILING DATE: 2001-12-18  
 PRIOR APPLICATION NUMBER: 10/055,569  
 PRIOR FILING DATE: 2001-10-26  
 PRIOR APPLICATION NUMBER: 10/080,334  
 PRIOR FILING DATE: 2002-02-21  
 PRIOR APPLICATION NUMBER: 10/092,900  
 PRIOR FILING DATE: 2002-03-07  
 PRIOR APPLICATION NUMBER: 10/136,826  
 PRIOR FILING DATE: 2002-05-01  
 PRIOR APPLICATION NUMBER: 10/236,417  
 PRIOR FILING DATE: 2002-09-06  
 PRIOR APPLICATION NUMBER: 60/345,092  
 PRIOR FILING DATE: 2002-01-04  
 Remaining Prior Application data removed - See File Wrapper or PALM.  
 NUMBER OF SEQ ID NOS: 12  
 SOFTWARE: CraraSeqist version 0.1  
 SEQ ID NO: 132  
 LENGTH: 309  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-336,472-132

Query Match 71.0%; Score 1149.5; DB 12; Length 309;  
 Best Local Similarity 72.2%; Pred. No. 3.5e-116;  
 Matches 226; Conservative 31; Mismatches 51; Indels 5; Gaps 3;

Qy	1 MVGLKSSDVPPMAVKLGACTAATADLVYPLPTAKVRLQIQLQNA-VOTARLYQYR	59
Db	1 MVGFKATDVPPVATVKLGACTAATDLYPLPTAKVRLQIQLQSGPVRATASQYR	60
Qy	60 GLSTLITMTRTEGRSPSPNVLVAGLQRQMSFASRIGJLQJDSKVQYTKPGADNSLTTR	119
Db	61 GNGTGTITMTRTEGRSPSPLNGVLVAGLQRQMSFASRIGJLQJDSKVQYTKPGADNSLTTR	119
Qy	120 ILAGCTTGAMAVTCAQPTDVKVRFOASIHGSPRSRSDRKSGTMDAIRTAREGGRLW	179
Db	120 ILAGCTTGAMAVTCAQPTDVKVRFOASIHGSPRSRSDRKSGTMDAIRTAREGGRLW	176
Qy	120 LLAGSTRGALAVAVQPTDVKVRFOAQRAG--GRRYOSTWAKTAREESPRGLW	176
Db	120 LLAGSTRGALAVAVQPTDVKVRFOAQRAG--GRRYOSTWAKTAREESPRGLW	176
Qy	180 KGTLPNMRNNAIVNCACBVEVTDILKEKLLDYLHLLTNPCHFVSATGGFCATVVASPVD	239
Db	177 KGTSPNVAARNIAVNCAELVTDILKODALKANLMDDLPCHTSARGAGCTTVIASPVD	236
Qy	240 VIKTRYNNSPQQYFSLDCMKVQAGEGPAFYKGFTPSLRLGSWNVMFVTEQQLR	299
Db	237 VIKTRYNNSALGOYSSGAGHCAUTMLQREGPRAFYKGFMPSFLRGSWNVVMFVTEQQLR	296
Qy	300 ALMKVQMLRESP 312	
Db	297 ALMABCSTSREAP 309	

RESULT 14  
 US-10-270-861-34  
 ; Sequence 34, Application US/10270861  
 ; General Information:  
 ; Sequence No.: US20030077749A1  
 ; Publication No.: US20030077749A1  
 ; Applicant: Adams, Sean  
 ; Applicant: Pan, James  
 ; Title of Invention: UCFS  
 ; File Reference: P1663R2  
 ; Current Application Number: US/10/270-861  
 ; Current Filing Date: 2002-10-15  
 ; Prior Application Number: US/09/433,622  
 ; Prior Filing Date: 1999-11-02  
 ; Prior Application Number: US 6/0/110,286  
 ; Prior Filing Date: 1998-11-30  
 ; Prior Application Number: US 60/129,583  
 ; Prior Application Number: US 60/129,583

300 ALMKVQMLRESP 312

PRIOR FILING DATE: 1999-04-16  
 PRIOR APPLICATION NUMBER: US 60/143,886  
 PRIOR FILING DATE: 1999-07-15  
 NUMBER OF SEQ ID NOS: 36  
 SEQ ID NO: 34  
 LENGTH: 309  
 TYPE: PRT  
 ORGANISM: Homo sapien  
 US-10-270-861-34

Query Match 71.0% Score 1149.5; DB 14; Length 309;  
 Best Local Similarity 72.2%; Pred. No. 3.5e-116; Mismatches 51; Indels 5; Gaps 3;  
 Matches 226; Conservative 31; Mismatches 51; Indels 5; Gaps 3;

QY 1 MVGSIKPSDVPPTMVAKPLAGTACFADLVTPLDTAKVRLQIOGESQQGPVATASQYR 59  
 Db 1 MVGPKATDVPPATVKFLGAGTACTADLITPLDTAKVRLQIOGESQQGPVATASQYR 59  
 Db 1 MVGPKATDVPPATVKFLGAGTACTADLITPLDTAKVRLQIOGESQQGPVATASQYR 60  
 QY 60 GVGTTILTMVRTRGPCCSPYNGLVAGLQRQMSAFASIRIGLYDYSVQVYTPKGADNSLITR 119  
 Db 61 GVGTGTTILTMVRTRGPCCSPYNGLVAGLQRQMSAFASIRIGLYDYSVQVYTPKGADNSLITR 119  
 QY 120 ILAGCTTGAMAVTCAQPDVVKRFOASITHGGRSRDKYSGTMDAYTIREGGVGLW 179  
 Db 120 ILAGSTTGALAVAVQAQTDPVVKRFOAQARAG--GGRYQSTVNAKYTIREEGVGLW 179  
 Db 120 ILAGSTTGALAVAVQAQTDPVVKRFOAQARAG--GGRYQSTVNAKYTIREEGVGLW 176  
 QY 180 KGTLPNMRNATNCABEVTYDILKEKUDYLITDNFPCHVSARGACPCATUVASVD 239  
 Db 177 KGTSPNVRNATNCABEVTYDILKEKUDYLITDNFPCHVSARGACPCATUVASVD 236  
 QY 240 VKTRYMSPPGQYFSPLDCMVKONAQEGPTIAFKGFTTSFLRUGSWANVVMFTYEQIKR 299  
 Db 237 VKTRYMSALQOYSSAGHCALTMLQKEGPRAFYKGFPMSFLRUGSWANVVMFTYEQIKR 296  
 Qy 300 ALMKVQMRBESPP 312  
 Db 297 ALMAACTSREAPP 309

RESULT 15  
 US-10-265-689-1  
 Sequence 1, Application US/10265689  
 Publication No. US20030119775A1

GENERAL INFORMATION:  
 APPLICANT: SURMIT, RICHARD S.  
 APPLICANT: COLLINS, SHEILA A.  
 APPLICANT: WARDEN, CRAIG H.  
 APPLICANT: SEIDIN, MICHAEL F.  
 APPLICANT: RICQUIER, DANIEL  
 APPLICANT: BOUILAUD, FREDERIC  
 TITLE OF INVENTION: RESPIRATION UNCOUPLING PROTEIN  
 FILE REFERENCE: 1579-376  
 CURRENT APPLICATION NUMBER: US/10/265,689  
 CURRENT FILING DATE: 2002-10-08  
 PRIOR APPLICATION NUMBER: US/09/353,645  
 PRIOR FILING DATE: 1999-07-15  
 PRIOR APPLICATION NUMBER: PCT/US97/06864  
 PRIOR FILING DATE: 1997-04-22  
 PRIOR APPLICATION NUMBER: 60/034,950  
 PRIOR FILING DATE: 1997-01-15  
 NUMBER OF SEQ ID NOS: 47  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 1  
 LENGTH: 309  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-265-689-1

Query Match 71.0% Score 1149.5; DB 14; Length 309;  
 Best Local Similarity 72.2%; Pred. No. 3.5e-116; Mismatches 51; Indels 5; Gaps 3;  
 Matches 226; Conservative 31; Mismatches 51; Indels 5; Gaps 3;

QY 1 MVGLKPSDVPPTMVAKPLAGTACFADLVTPLDTAKVRLQIOGESQQGPVATASQYR 59



CC of adipose mass and maintenance of the lean mass) in all types of obesity by promoting the dissipation of energy; for preventing an excessive weight regain following restrictive food diet or after ceasing a physical training programme; for preventing and treating type II diabetes by improving sensitivity to insulin; for preventing hypertension; for increasing muscle mass in states of cachexia; for treatment of insufficiencies or disturbances of cardiac rhythm due to a dysfunction of UCP-3; and for the treatment of neuromuscular diseases due to a dysfunction of UCP3. The uncoupling proteins can also be used to raise antibodies, e.g. for diagnosis. Knowledge of the UCP3 genes allows generation of transgenic animals, e.g. for screening substances which modify UCP3 expression or activity or for investigating the biological role of UCP3.

XX Sequence 312 AA;

Query Match 100.0%; Score 1620; DB 2; Length 312; Best Local Similarity 100.0%; Pred. No. 2.2e-165; Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0; CC

Qy 1 MVGLKPSDVPTMAVKELGAGTAACFADLVTPLDTAKVRVQIQGENQAVQVATRLVQYRG 60

Db 1 MVGLKPSDVPTMAVKELGAGTAACFADLVTPLDTAKVRVQIQGENQAVQVATRLVQYRG 60

Qy 61 VLGTTLMVRTEGCPSPYNGLAGIQRQMSAIGRIGLYDVSQVYTPKGADNSSLTRI 120

Db 61 VLGTTLMVRTEGCPSPYNGLAGIQRQMSAIGRIGLYDVSQVYTPKGADNSSLTRI 120

Qy 121 LAGCTTGAMATCAQOPTDVVKURFOASHIHLGSPRSRDRKSYGTMDAYRTIARREGRLWK 180

Db 121 LAGCTTGAMATCAQOPTDVVKURFOASHIHLGSPRSRDRKSYGTMDAYRTIARREGRLWK 180

Qy 181 GTLPNIMRNATAVCAEVTVYDILKEKLDDYLHTDNFPCHIVSAFGAGFCATVVASPVD 240

Db 181 GTLPNIMRNATAVCAEVTVYDILKEKLDDYLHTDNFPCHIVSAFGAGFCATVVASPVD 240

Qy 241 VCKTRVNSPPQQYFSPLDCMKVNAQEGPTAFLYKGFTPSRFLGSWNVMFTYFQLKRA 300

Db 241 VCKTRVNSPPQQYFSPLDCMKVNAQEGPTAFLYKGFTPSRFLGSWNVMFTYFQLKRA 300

Qy 301 LMKVQMLRESPF 312

Db 301 LMKVQMLRESPF 312

RESULT 2

ID AAW68197

ID AAW68197 standard; protein: 312 AA.

AC AAW68197;

DT 07-DEC-1998 (first entry)

XX Human uncoupling protein HNPCW60.

XX HNPCW60; uncoupling protein; human; body weight disorder; obesity; diabetes; hyperlipidaemia; diagnosis; therapy; vaccine.

OS Homo sapiens.

PN WO9839432-A1.

XX 11-SEP-1998.

PD 02-MAR-1998; 98WO-GB000633.

PR 05-MAR-1997; 97GB-00004551.

PR 18-MAR-1997; 97GB-00005614.

PR 16-JUL-1997; 97EP-00305305.

XX (SMIK ) SMITHKLINE BEECHAM PLC.

PA Beeley LJ, Paine K, Godden RJ;

PI

XX WPI; 1998-495841/42.

DR N-PSDB; AAV54602.

XX DR

XX PT New isolated human uncoupling poly-peptide(s) - used to develop products for the diagnosis, prevention and treatment of body weight disorders, obesity and diabetes.

XX PT

XX BS Claim 4; Page 24-25; 41pp; English.

XX X

CC This is the amino acid sequence of novel human uncoupling protein HNFCW60, as deduced from an isolated polynucleotide (see AAV54602). The invention relates to HNFCW60 polypeptides and recombinant materials and methods for their production. It also relates to methods for using such HNFCW60 polypeptides and polynucleotides. Such uses include the treatment of obesity, hyperlipidaemia and body weight disorders. The invention also provides methods of identifying agonists and antagonists, and methods for treating conditions associated with HNFCW60 imbalance using the identified compounds. In addition, diagnostic assays for detecting diseases associated with inappropriate HNFCW60 activity or levels are provided.

XX X

Sequence 312 AA;

Query Match 100.0%; Score 1620; DB 2; Length 312; Best Local Similarity 100.0%; Pred. No. 2.2e-165; Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0; CC

Qy 1 MVGLKPSDVPTMAVKELGAGTAACFADLVTPLDTAKVRVQIQGENQAVQVATRLVQYRG 60

Db 1 MVGLKPSDVPTMAVKELGAGTAACFADLVTPLDTAKVRVQIQGENQAVQVATRLVQYRG 60

Qy 61 VLGTTLMVRTEGCPSPYNGLAGIQRQMSAIGRIGLYDVSQVYTPKGADNSSLTRI 120

Db 61 VLGTTLMVRTEGCPSPYNGLAGIQRQMSAIGRIGLYDVSQVYTPKGADNSSLTRI 120

Qy 121 LAGCTTGAMATCAQOPTDVVKURFOASHIHLGSPRSRDRKSYGTMDAYRTIARREGRLWK 180

Db 121 LAGCTTGAMATCAQOPTDVVKURFOASHIHLGSPRSRDRKSYGTMDAYRTIARREGRLWK 180

Qy 181 GTLPNIMRNATAVCAEVTVYDILKEKLDDYLHTDNFPCHIVSAFGAGFCATVVASPVD 240

Db 181 GTLPNIMRNATAVCAEVTVYDILKEKLDDYLHTDNFPCHIVSAFGAGFCATVVASPVD 240

Qy 241 VCKTRVNSPPQQYFSPLDCMKVNAQEGPTAFLYKGFTPSRFLGSWNVMFTYFQLKRA 300

Db 241 VCKTRVNSPPQQYFSPLDCMKVNAQEGPTAFLYKGFTPSRFLGSWNVMFTYFQLKRA 300

Qy 301 LMKVQMLRESPF 312

Db 301 LMKVQMLRESPF 312

RESULT 3

ID AAW85667

ID AAW85667 standard; protein: 312 AA.

XX AC AAW85667;

XX DT 19-JUL-1999 (first entry)

XX Human UCP-3 (uncoupling protein).

XX UCP-3; uncoupling protein; thermogenesis; skeletal muscle; treatment; obesity; diabetes; hyperthermia; fever; detection; diagnosis.

OS Homo sapiens.

XX WO9845313-A1.

XX PD 15-OCT-1998.

XX PP 25-MAR-1998; 98WO-US0005892.

XX	PR	04-APR-1997;	97US-0043407P.
XX	PR	08-MAY-1997;	97US-0046154P.
XX	PR	08-MAY-1997;	97US-0047179P.
XX	PR	09-AUG-1997;	97GB-00016886.
XX	PR	09-DEC-1997;	97US-0069141P.
XX	PA	(AMYL- ) AMYLIN PHARM INC.	
XX	PT	Larkin S., Moore C., Albrandt K., Young A., Beaumont K.; WPI; 1999-131682/11.	
XX	PT	New isolated uncoupling protein, UCP3 - used to develop products for modulating thermogenesis in tissues, e.g. for treating obesity, diabetes, malignant hyperthermia or fever.	
XX	PT	Claim 4; Fig 5; 97pp; English.	
XX	PS	The uncoupling protein UCP-3 is involved in thermogenesis and energy utilisation in skeletal muscle. The nucleic acid molecule encoding UCP-3 or compounds which activate UCP-3 can be used to increase thermogenesis in a subject, e.g. for treating obesity or for decreasing the amount of fat in a subject. They can also be used for treating diabetes. Compounds which inhibit UCP-3 activation in tissues of a subject can be used for decreasing thermogenesis or respiratory ATP synthesis e.g. for preventing or treating malignant hyperthermia or fever. The UCP-3 can also be used for screening for compounds that bind to or modulate the activity of UCP-3, these compounds can then be used in detection and diagnosis	
XX	SQ	Sequence 312 AA;	
CC	Query Match	100.0%: Score 1620; DB 2; Length 312;	
CC	Best Local Similarity	100.0%; Pred. No. 2, 2e-165;	
CC	Matches	312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1	MVGILKPSDVPPTMKFLGAGTACFADLVTFLDFTAKVRLQIOPENAVQTVRLVQRG 60	
Db	1	MVGILKPSDVPPTMKFLGAGTACFADLVTFLDFTAKVRLQIOPENAVQTVRLVQRG 60	
OY	61	VIGLTILMWRTEGPCSPNGLVAGLQRQMSAFASIRIGLYDSVKQVYTPKGADNSLITRI 120	
Db	61	VIGLTILMWRTEGPCSPNGLVAGLQRQMSAFASIRIGLYDSVKQVYTPKGADNSLITRI 120	
OY	121	LACCTTGAMAVTCQPTWVKRFOASHLGPSPRSDRKYSGMDAYRTIAREGVGRGLWK 180	
Db	121	LACCTTGAMAVTCQPTWVKRFOASHLGPSPRSDRKYSGMDAYRTIAREGVGRGLWK 180	
OY	181	GTLPNIMRNVAIVCAEVVYDIKEKLADYHLLTDNFPCFHVSFAFGAGCATWASPDV 240	
Db	181	GTLPNIMRNVAIVCAEVVYDIKEKLADYHLLTDNFPCFHVSFAFGAGCATWASPDV 240	
OY	241	VKTRYMNNSPPGQYFSPLDCMIKOMVAQEGPTAFYKGFITSFLRGWSWNVMFVTYBOLKRA 300	
Db	241	VKTRYMNNSPPGQYFSPLDCMIKOMVAQEGPTAFYKGFITSFLRGWSWNVMFVTYBOLKRA 300	
OY	301	LMKVQLMLRSPP 312	
Db	301	LMKVQLMLRSPP 312	
RESULT 4	A8W8219	A8W8279 standard; protein; 312 AA.	
ID	OY	1	MVGILKPSDVPPTMKFLGAGTACFADLVTFLDFTAKVRLQIOPENAVQTVRLVQRG 60
AC	Db	1	MVGILKPSDVPPTMKFLGAGTACFADLVTFLDFTAKVRLQIOPENAVQTVRLVQRG 60
XX	DT	12-APR-1999 (first entry)	
DE	Human uncoupling protein 3 (UCP3).		
KW	Uncoupling Protein 3; UCP3; human; obesity; diabetes; hyperinsulinaemia; hypermetabolism; therapy.		
KW	OS Homo sapiens.		
XX	PR	04-APR-1997;	97US-0043407P.
XX	PR	08-MAY-1997;	97US-0046154P.
XX	PR	08-AUG-1997;	97GB-00016886.
XX	PR	09-DEC-1997;	97US-0069141P.
XX	PA	(MERCK ) MERCK & CO INC.	
XX	PT	Liu Q., Chen F.; WPI; 1999-059737/5.	
XX	DR	N-PSDB; AAV84254.	
XX	PT	New isolated human uncoupling protein 3 - used to identify compounds which can modulate energy expenditure and body weight regulation, e.g. in the treatment of obesity or diabetes.	
XX	PS	Claim 3; Page 58; 87pp; English.	
XX	CC	This is human uncoupling protein 3 (UCP3), a novel protein that is involved in energy expenditure and body weight regulation and whose expression is mostly limited to skeletal muscle. The amino acid sequence was deduced from the nucleotide sequence of an isolated foetal brain cDNA clone (see AAV8454). The invention additionally provides related recombinant expression vectors and recombinant host cells. UCP3 polypeptides and transformed recombinant cell lines can be used for identifying modulators of UCP3 activity. The modulators can be used for treating diseases such as obesity and diabetes, by manipulating the interrelated process of balancing food intake, energy expenditure and glucose metabolism within the patient. They can also be used to treat hyperactive conditions of energy expenditure which originate in the mitochondria of skeletal muscle. UCP3 nucleic acids are useful in gene therapy of obesity and obesity-related indications, including diabetes, and of mitochondrial-associated hypermetabolism.	
XX	SQ	Sequence 312 AA;	
CC	Query Match	100.0%: Score 1620; DB 2; Length 312;	
CC	Best Local Similarity	100.0%; Pred. No. 2, 2e-165;	
CC	Matches	312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1	MVGILKPSDVPPTMKFLGAGTACFADLVTFLDFTAKVRLQIOPENAVQTVRLVQRG 60	
Db	61	VIGLTILMWRTEGPCSPNGLVAGLQRQMSAFASIRIGLYDSVKQVYTPKGADNSLITRI 120	
OY	121	LACCTTGAMAVTCQPTWVKRFOASHLGPSPRSDRKYSGMDAYRTIAREGVGRGLWK 180	
Db	61	VIGLTILMWRTEGPCSPNGLVAGLQRQMSAFASIRIGLYDSVKQVYTPKGADNSLITRI 120	
OY	181	GTLPNIMRNVAIVCAEVVYDIKEKLADYHLLTDNFPCFHVSFAFGAGCATWASPDV 240	
Db	181	GTLPNIMRNVAIVCAEVVYDIKEKLADYHLLTDNFPCFHVSFAFGAGCATWASPDV 240	
OY	241	VKTRYMNNSPPGQYFSPLDCMIKOMVAQEGPTAFYKGFITSFLRGWSWNVMFVTYBOLKRA 300	
Db	241	VKTRYMNNSPPGQYFSPLDCMIKOMVAQEGPTAFYKGFITSFLRGWSWNVMFVTYBOLKRA 300	
OY	301	LMKVQLMLRSPP 312	
Db	301	LMKVQLMLRSPP 312	
RESULT 5	AAV31904		

			Db	181 GTLPIMMRNAINVNCLEVVYDILKEKLLYHLLTDNPCHFVSAFGAGCATTAVASPVV 240
XX			Qy	241 VKTRYMNNSPPGQYFSPLDEMIVKMYAQEGPFTAFYKGFTSPFLRLSASWNVMFVTBOLKRA 300
AC			Db	241 VKTRYMNNSPPGQYFSPLDEMIVKMYAQEGPFTAFYKGFTSPFLRLSASWNVMFVTBOLKRA 300
XX			Qy	301 LMKVQMLRSPF 312
DT			Db	301 LMKVQMLRSPF 312
XX				
DB	Human uncoupling protein 3.			
XX	Uncoupling protein 3; UCP3; human; obesity; diabetes; diagnosis;			
KW	gene therapy.			
XX	Homo sapiens.			
OS				
XX				
FH	Key difference Location/Qualifiers			
FT	Misc-difference 70 /note= "substituted by Trp in C208T polymorphism"			
FT	Misc-difference 102 /note= "substituted by Val in G300A polymorphism"			
FT	Misc-difference 142 /note= "C-terminal residue in C427T polymorphism"			
FT				
XX				
PN	WO9948905-A1.			
XX				
PD	30-SEP-1999.			
XX				
PP	23-MAR-1999; 99WO-US006317.			
XX				
PR	23-MAR-1998; 98US-0078972P.			
XX				
PA	(MUSC-) MUSC FOUND RES DEV.			
XX				
PA	Garvey WT, Argyropoulos G;			
XX				
DR	WPI; 1999-591072/50.			
N-PSDB; AA219969.				
XX				
PT	Use of uncoupled protein 2 or 3 as markers for identifying subjects at risk of developing obesity or diabetes.			
XX				
PS	Disclosure; Page 103-104; 112pp; English.			
XX				
CC	The present sequence represents human uncoupling protein 3 (UCP3). The invention relates to the discovery that the presence of a single nucleotide polymorphism (SNP) in a nucleic acid encoding UCP3 (see AAC19969) or UCP2 (see AA219968) can correlate with the development of obesity and type II diabetes mellitus. In UCP3, the SNP may generate a Trp for Arg substitution at position 70 of the encoded protein, a protein truncated after residue 142, or a Val for Ile substitution at position 102. Methods are provided for identifying a subject at risk of developing obesity and/or diabetes by detection of the SNP in the UCP2/UCP3 nucleic acid or amino acid sequence. An antibody to an antigen of the altered UCP2 can be used in such a method			
SO	Sequence 312 AA;			
Query Match	100.0%; Score 1620; DB 2; Length 312;			
Best Local Similarity	100.0%; Pred. No. 2.2e-165;			
Matches	312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Ov	1 MWGLKPSDVPTPKVAKELGAGTAACFADLVTFLDTAKVRLQIQGENQAVQAVTARLYQRG 60			
Db	1 VLGTLTMRTECPSPCGNLYGIGLORMSFASIRIGLYSYKQVTPKGADNSLITRI 120			
Db	1 MWGLKPSDVPTPKVAKELGAGTAACFADLVTFLDTAKVRLQIQGENQAVQAVTARLYQRG 60			
Db	61 VLGTLTMRTECPSPCGNLYGIGLORMSFASIRIGLYSYKQVTPKGADNSLITRI 120			
Db	61 VLGTLTMRTECPSPCGNLYGIGLORMSFASIRIGLYSYKQVTPKGADNSLITRI 120			
Qy	1 MWGLKPSDVPTPKVAKELGAGTAACFADLVTFLDTAKVRLQIQGENQAVQAVTARLYQRG 60			
Qy	121 LAGCTTGAMVTAQOPTDVKVRPOASHTLGPSSDRKYSGTMDAYTIAAREGVGLWK 180			
Db	121 LAGCTTGAMVTAQOPTDVKVRPOASHTLGPSSDRKYSGTMDAYTIAAREGVGLWK 180			
Qy	181 GTLPIMMRNAINVNCLEVVYDILKEKLLYHLLTDNPCHFVSAFGAGCATTAVASPVV 240			
Qy	61 VLGTLTMRTECPSPCGNLYGIGLORMSFASIRIGLYSYKQVTPKGADNSLITRI 120			
Qy	1 MWGLKPSDVPTPKVAKELGAGTAACFADLVTFLDTAKVRLQIQGENQAVQAVTARLYQRG 60			
Db	1 MWGLKPSDVPTPKVAKELGAGTAACFADLVTFLDTAKVRLQIQGENQAVQAVTARLYQRG 60			

Db	61	VIGTILIVWRTEGPGCSPYNGLVAGLQRQMSFASIRGLYDVKQVTPKGADNSLTRI	120	OY	1	MUJLKPSDVPTMAVKELGAGTAACFADEPLDPAKVRLOIQLGENAQVTARIWYRG	60
OY	121	LAGCTTGAMAVCAQPTDVVKRFOASHLHGSRSRDKYSGTMDAYTARBEVGRLWK	180	DB	1	WYGLKESDVPPTMAVKELGAGTAACFADEPLDPAKVRLOIQLGENAQVTARIWYRG	60
Db	121	LAGCTTGAMAVCAQPTDVVKRFOASHLHGSRSRDKYSGTMDAYTARBEVGRLWK	180	OY	61	VIGTILIVWRTEGPGCSPYNGLVAGLQRQMSFASIRGLYDVKQVTPKGADNSLTRI	120
OY	181	GTLPNMENAINCAEVUTYDILKEKLDYLHLLTDNTPCHFVSAFGAGFCATWASPDV	240	DB	61	VIGTILIVWRTEGPGCSPYNGLVAGLQRQMSFASIRGLYDVKQVTPKGADNSLTRI	120
Db	181	GTLPNMENAINCAEVUTYDILKEKLDYLHLLTDNTPCHFVSAFGAGFCATWASPDV	240	OY	121	LAGCTTGAMAVCAQPTDVVKRFOASHLHGSRSRDKYSGTMDAYTARBEVGRLWK	180
OY	241	VKTRYMSPPGQYFSPDCMIIKVAQEGPTAFYKGFTSPFLRGSWNVUMFTYBOKRA	300	DB	121	LAGCTTGAMAVCAQPTDVVKRFOASHLHGSRSRDKYSGTMDAYTARBEVGRLWK	180
Db	241	VKTRYMSPPGQYFSPDCMIIKVAQEGPTAFYKGFTSPFLRGSWNVUMFTYBOKRA	300	OY	181	GTLPNMENAINCAEVUTYDILKEKLDYLHLLTDNTPCHFVSAFGAGFCATWASPDV	240
OY	301	LMKVQMLRESPF	312	DB	181	GTLPNMENAINCAEVUTYDILKEKLDYLHLLTDNTPCHFVSAFGAGFCATWASPDV	240
Db	301	LMKVQMLRESPF	312	OY	241	VKTRYMSPPGQYFSPDCMIIKVAQEGPTAFYKGFTSPFLRGSWNVUMFTYBOKRA	300
<b>RESULT 7</b>							
AY44253	ID	AY44253	standard; protein; 312 AA.	301	LMKVQMLRESPF	312	OY
XX	AC	AY44253;		301	LMKVQMLRESPF	312	DB
XX	DT	28-FEB-2000	(first entry)				
XX	DE	Human mitochondrial anion carrier, uncoupling protein-3.					
XX	KW	Mitochondrial uncoupling protein-3; UCP-3; mitochondrial anion carrier; MAC; modulator; transport protein; fatty acid anion; mitochondria; assay vesicle; metabolic disorder; diabetes; obesity; cancer; human.					
XX	OS	Homo sapiens.					
XX	PN	WO9964458-A1.					
XX	PD	16-DEC-1999.					
XX	PP	99WO-US012623.					
XX	PR	08-JUN-1998; 98US-00093662.					
XX	PA	(TYBO-) UNIV BOSTON.					
XX	PI	Corkey BB, Hamilton JA, Pilch PF, Farmer SR, Kirkland JL;					
XX	DR	WPI; 2000-087200/07.					
XX	DR	N-PSDB; A2Z9245.					
XX	PT	Identifying modulators of mitochondrial anion carriers, potentially useful for treating metabolic disease, e.g. diabetes and obesity.					
XX	PS	Claim 11; Page 73-74; 80pp; English.					
XX	CC	The present sequence is a human uncoupling protein-3 (UCP-3) which is a mitochondrial anion carrier (MAC). The UCPS transport free fatty acid anions across the inner mitochondrial membrane to induce cyclical proton movement. This transport is tightly related to oxidation of fatty acids in the mitochondria, thereby converting fatty acids into energy rather than storing them. The uncoupling protein is used in the preparation of assay vesicles that are used to identify modulators of MAC activity. MAC modulators are useful for treating metabolic disorders, particularly diabetes and obesity. Modulators that act as inhibitors can be used to treat conditions requiring a reduction in energy expenditure, e.g. in cancer patients or the elderly.					
SQ	Sequence 312 AA;						
Query Match	100.0%	Score 1620; DB 3;	Length 312;	Query Match	100.0%	Score 1620; DB 4;	Length 312;
Best Local Similarity	100.0%;	Pred. No. 2.2e-165;		Best Local Similarity	100.0%;	Pred. No. 2.2e-165;	
Matches	312;	Conservative	0;	Matches	312;	Mismatches	0;
		Indels	0;			Gaps	0;

QY 1 MVGLKPSDVPTMAVKFLGAGTAACPAIDLVTPLDTAKVRIQIQENAOVQATARIVQRG 60  
 XX 1 MVGLKPSDVPTMAVKFLGAGTAACPAIDLVTPLDTAKVRIQIQENAOVQATARIVQRG 60  
 QY 61 VLTGILTMVRTEGCPSPYNGLVAGLQRQMSHASFIRIGLYPSVKQVTPKGADNSLLTRI 120  
 XX 61 VLTGILTMVRTEGCPSPYNGLVAGLQRQMSHASFIRIGLYPSVKQVTPKGADNSLLTRI 120  
 Db 121 LAGCTTGAMAVTCQAOPTDVVKURFOASHIHGPSRSRKYSDRKGTYMAYTIREEGRLWK 180  
 XX 121 LAGCTTGAMAVTCQAOPTDVVKURFOASHIHGPSRSRKYSDRKGTYMAYTIREEGRLWK 180  
 Db 181 GTLPNIMRNAVNCAEVTVTIDILEKLDVHLTNFPCFVSAFGAGFCATVVASPVD 240  
 XX 181 GTLPNIMRNAVNCAEVTVTIDILEKLDVHLTNFPCFVSAFGAGFCATVVASPVD 240  
 QY 241 VKTRYNNSPGQYFSPLDCMKVNAQEGPTAFYKGFTPSFLRLGSWNVMFVTEQLRA 300  
 XX 241 VKTRYNNSPGQYFSPLDCMKVNAQEGPTAFYKGFTPSFLRLGSWNVMFVTEQLRA 300  
 Qy 301 LMKVQMLRESPF 312  
 XX 301 LMKVQMLRESPF 312

**RESULT 9**  
 ID AAE04298 standard; protein; 312 AA.  
 AC AAE04298;  
 XX  
 DT 04-SEP-2001 (first entry)  
 DB Human uncoupling protein-3 (UCP3).  
 KW Human; UCP3; uncoupling protein-3; chromosome 11q3; gene therapy;  
 KW atherosclerosis; hypercholesterolaemia; antilipemic.  
 OS Homo sapiens.  
 PR WO200143760-A2.  
 XX 21-JUN-2001.  
 PD XX  
 PP 18-DEC-2000; 2000WO-EP012931.  
 XX  
 PR 17-DEC-1999; 99GB-00030100.  
 XX (SMIK ) SMITHKLINE BEECHAM PLC.  
 PA Clapham JC;  
 PI  
 DR WPI; 2001-398073/42.  
 XX N-PSDB; AAB08530.

PT Use of a compound selected from UCP3 polypeptide, a compound which activates the polypeptide, or a polynucleotide encoding the polypeptide, for treating atherosclerosis or hypercholesterolaemia.

XX  
 PS Claim 5; Page 19; 24pp; English.

The present sequence is human UCP3 (uncoupling protein-3) protein. UCP3 gene is located in chromosome 11q3. UCP3 protein and polynucleotides encoding them are useful for identifying agonist compounds which are potentially useful in therapy. UCP3 protein is useful for inducing an immunological response, as an immunogen to produce antibodies immunospecific for UCP3 protein, and in a method for the structure-based design of an agonist of UCP3 protein. UCP3 sequences are useful to configure screening methods for detecting the effect of added components on the production of mRNA and polypeptide in cells. UCP3 DNA is used in gene therapy. A compound which activates UCP3 protein or a polynucleotide encoding UCP3 protein are used for the manufacture of medicament for treating

CC atherosclerosis or hypercholesterolaemia  
 XX  
 Sequence 312 AA;

Query Match 100.0%; Score 1620; DB 4; Length 312;  
 Best Local Similarity 100.0%; Prd. No. 2.2e-165;  
 Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MVGLKPSDVPTMAVKFLGAGTAACPAIDLVTPLDTAKVRIQIQENAOVQATARIVQRG 60  
 XX 1 MVGLKPSDVPTMAVKFLGAGTAACPAIDLVTPLDTAKVRIQIQENAOVQATARIVQRG 60  
 Db 121 LAGCTTGAMAVTCQAOPTDVVKURFOASHIHGPSRSRKYSDRKGTYMAYTIREEGRLWK 180  
 XX 121 LAGCTTGAMAVTCQAOPTDVVKURFOASHIHGPSRSRKYSDRKGTYMAYTIREEGRLWK 180  
 Db 61 VLTGILTMVRTEGCPSPYNGLVAGLQRQMSHASFIRIGLYPSVKQVTPKGADNSLLTRI 120  
 XX 61 VLTGILTMVRTEGCPSPYNGLVAGLQRQMSHASFIRIGLYPSVKQVTPKGADNSLLTRI 120  
 Db 181 GTLPNIMRNAVNCAEVTVTIDILEKLDVHLTNFPCFVSAFGAGFCATVVASPVD 240  
 XX 181 GTLPNIMRNAVNCAEVTVTIDILEKLDVHLTNFPCFVSAFGAGFCATVVASPVD 240  
 QY 121 LAGCTTGAMAVTCQAOPTDVVKURFOASHIHGPSRSRKYSDRKGTYMAYTIREEGRLWK 180  
 XX 121 LAGCTTGAMAVTCQAOPTDVVKURFOASHIHGPSRSRKYSDRKGTYMAYTIREEGRLWK 180  
 Db 181 GTLPNIMRNAVNCAEVTVTIDILEKLDVHLTNFPCFVSAFGAGFCATVVASPVD 240  
 XX 181 GTLPNIMRNAVNCAEVTVTIDILEKLDVHLTNFPCFVSAFGAGFCATVVASPVD 240  
 Qy 181 GTLPNIMRNAVNCAEVTVTIDILEKLDVHLTNFPCFVSAFGAGFCATVVASPVD 240  
 Db 301 LMKVQMLRESPF 312  
 XX 301 LMKVQMLRESPF 312

**RESULT 10**  
 ID AAB6050  
 AC AAB6050 standard; protein; 312 AA.  
 XX  
 AC AAB6050;  
 XX  
 DT 29-JUN-2001 (first entry)  
 XX  
 DE Amino acid sequence of a human uncoupling protein 3 (UCP3).  
 KW Uncoupling protein 3; UCP3; transgenic rodent; UCP3-related disease; obesity; diabetes; hyperlipidemia; body weight disorder; wound healing; cachexia; inflammation; tissue repair; atherosclerosis.  
 OS Homo sapiens.  
 XX WO200124625-A1.  
 XX  
 PR 12-APR-2001.  
 XX  
 PR 29-SEP-2000; 2000WO-GB003747.  
 XX  
 PR 01-OCT-1999; 99GB-00023334.  
 XX (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX  
 PR Abuin A, Clapham J;  
 XX  
 DR WPI; 2001-273534/28.  
 DR N-PSDB; AAB84745.

New transgenic rodent, useful for determining phenotypic effect of a compound, comprises a polynucleotide encoding a human uncoupling protein 3 under control of regulatory sequence in its genome.

XX Disclosure; Page 24-25; 28pp; English.

The present sequence represents a human uncoupling protein 3 (UCP3). The UCP3 polynucleotide is used to produce a transgenic rodent comprising a UCP3 polynucleotide in its genome, under the control of a regulatory

CC sequence facilitating the expression of the polypeptide. The transgenic rodent is useful for determining the phenotyping effect of a compound, which may be used for treating UC3-related disease such as obesity, diabetes, hyperlipidemia, body weight disorders, wound healing, cachexia, inflammation and tissue repair of atherosclerosis. The transgenic mice expressing human UC3 have significantly reduced body weight compared to age-matched wild-type controls despite showing increased food intake, and thus are suitable for studies of body weight disorders, diabetes, obesity and inflammation and the evaluation of compounds that have potential to treat such diseases and disorders. The transgenic rodents are also useful for validation of the polypeptide expressed from the transgene as a drug target in addition to elucidating the function of a gene of interest. The transgenic rodents can also be used to test the efficacy of drug and drug administration regime for treating the above mentioned disorders and to investigate the effects of various drug treatments on the course of the disease.

XX Sequence 312 AA;

SQ

Query Match

100.0%; Score 1620; DB 4;

Length 312;

Best Local Similarity

100.0%; Pred. No. 2;

2e-165;

Mismatches 0;

Indels 0;

Gaps 0;

Matches 312;

Conservative 0;

PS

CC

PR

XK

PR

XK

(CAPL/)

CARPLAN S L.

PA

(BOET/)

BOETTCHER B R.

PA

(SLOS/)

SLOSBERG E D.

PA

(CONN/)

CONNELLY S.

PA

(KALE/)

KALEKO M.

PA

(DESA/)

DESAI U J.

XK

Pi

Caplan SL,

Boettcher BR,

Slosberg ED,

Connelly S,

Kaleko M;

PT

Desai UJ;

XK

DR

N-PSDB;

ABQ72999.

XK

PT

Treating condition related to elevated blood glucose levels, especially diabetes or obesity, involves administering polynucleotide sequence encoding glucokinase regulatory protein, to a subject.

XK

PS

Disclosure; Page 16-17; 42pp; English.

XK

CC

CC

CC

CC

CC

CC

XK

15-MAR-2000; 2000US-0266328P.

PR

XK

(CAPL/)

CARPLAN S L.

PA

(BOET/)

BOETTCHER B R.

PA

(SLOS/)

SLOSBERG E D.

PA

(CONN/)

CONNELLY S.

PA

(KALE/)

KALEKO M.

PA

(DESA/)

DESAI U J.

XK

Pi

Caplan SL,

Boettcher BR,

Slosberg ED,

Connelly S,

Kaleko M;

PT

Desai UJ;

XK

DR

N-PSDB;

ABQ72999.

XK

PT

Treating condition related to elevated blood glucose levels, especially diabetes or obesity, involves administering polynucleotide sequence encoding glucokinase regulatory protein, to a subject.

XK

PS

Disclosure; Page 16-17; 42pp; English.

XK

CC

PR

XK

PR

XK

(CAPL/)

CARPLAN S L.

PA

(BOET/)

BOETTCHER B R.

PA

(SLOS/)

SLOSBERG E D.

PA

(CONN/)

CONNELLY S.

PA

(KALE/)

KALEKO M.

PA

(DESA/)

DESAI U J.

XK

DT

20-SEP-2002 (first entry)

XX

AC

ABB81610;

AC

PR

XK

PR

XK

(CAPL/)

CARPLAN S L.

PA

(BOET/)

BOETTCHER B R.

PA

(SLOS/)

SLOSBERG E D.

PA

(CONN/)

CONNELLY S.

PA

(KALE/)

KALEKO M.

PA

(DESA/)

DESAI U J.

XK

DT

20-SEP-2002 (first entry)

XX

AC

ABB81610;

AC

<div data-bbox="106 31 117 13



CC be used for inhibiting protein catabolism in a mammal such as inhibiting  
 CC muscle wasting. They can be used for curtailing muscle wasting due to  
 CC infection (e.g. HIV), cancer, tumour cachexia, muscle diseases (e.g.  
 CC muscular dystrophy) or as a possible treatment for non-insulin dependent  
 CC diabetes mellitus. The products can also be used for detection and  
 XX diagnosis.

SQ Sequence 312 AA;

Query Match 99.8%; Score 1616; DB 2; Length 312;  
 Beat Local Similarity 99.7%; Pred. No. 5.9e-165; 1; Mismatches 0; Indels 0; Gap 0;  
 Matches 311; Conservative 1;

Qy 1 MVGLKPSDVPPTMAYKFLGAGTAACTADLYTFPLDTAKVLQIOPENAQAVTARLVOYRG 60  
 Db 1 MVGLKPSDVPPTMAYKFLGAGTAACTADLYTFPLDTAKVLQIOPENAQAVTARLVOYRG 60  
 Qy 61 VLGTTILMVRTEGPSPYNGIVAGLQRQMSASIRGSPRSRKYSCMDAATRIBEGVGLWK 120  
 Db 61 VLGTTILMVRTEGPSPYNGIVAGLQRQMSASIRGSPRSRKYSCMDAATRIBEGVGLWK 120  
 Qy 121 LAGCTGAMAVTAOPTDVKVRFOASHINGPSPRSRKYSCMDAATRIBEGVGLWK 180  
 Db 121 LAGCTGAMAVTAOPTDVKVRFOASHINGPSPRSRKYSCMDAATRIBEGVGLWK 180  
 Qy 181 GTLPNIMRNATVCAEVTVTDILKEKLDYLTONPPCHEVSAGFCATVVASPVDV 240  
 Db 181 GTLPNIMRNATVCAEVTVTDILKEKLDYLTONPPCHEVSAGFCATVVASPVDV 240  
 Qy 241 VKTRYMSSPGQYFSLDCMIKVAQEGPTAFYKGFTPSFLRLGSNNVMFTYBOLKRA 300  
 Db 241 VKTRYMSSPGQYFSLDCMIKVAQEGPTAFYKGFTPSFLRLGSNNVMFTYBOLKRA 300  
 Qy 301 LMKVQMLRESPF 312  
 Db 301 LMKVQMLRESPF 312

RESULT 14

AAW81587

ID AAW81587 standard; protein; 312 AA.

AC AAW81587;

XX DT 09-FEB-1999 (first entry)

DE Human uncoupling protein 3 (UCP3).

XX Ucoupling protein 3; UCP3; thermogenesis; mammal; enhancer; drug;  
 KW protein catabolism; anti-obesity; inhibitor; muscle wasting; muscular dystrophy;  
 KW HIV; cancer; tumour cachexia; muscle disease; non-insulin dependent diabetes mellitus; diagnosis; human.

OS Homo sapiens.

XX WO9845438-A1.

PN XX

XX PD 15-OCT-1998.

XX PR 08-APR-1998; 98WO-US005959.

XX PR 09-APR-1997; 97US-0043447P.  
 PR 12-MAY-1997; 97US-0046254P.  
 PR 15-JUL-1997; 97US-00892745.

XX PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

XX Lowell BB, Flier JS;

XX WPI: 1998-594483/50.

DR N-PSDB; AAV71710.

XX PT New isolated uncoupling protein, UCP-3 - used to develop products for modulating thermogenesis in tissues, e.g. for treating obesity or muscle wasting caused by infection or cancer.

XX PS Claim 5; Fig 1A-C; 98PP; English.

XX This represents a human uncoupling protein 3 (UCP3). A host cell transformed with a construct comprising the UCP3 nucleic acid can be used for the recombinant production of the protein. The UCP3 is involved in the regulation of thermogenesis in mammals. The nucleic acids (AAV71710 to AAV71712) can be used for identifying compounds which alter UCP3 activity. Enhancers of UCP3 can be used for enhancing protein catabolism in a mammal and can be used as anti-obesity drugs. Inhibitors of UCP3 can

CC be used for inhibiting protein catabolism in a mammal such as inhibiting  
 CC muscle wasting. They can be used for curtailing muscle wasting due to  
 CC infection (e.g. HIV), cancer, tumour cachexia, muscle diseases (e.g.  
 CC muscular dystrophy) or as a possible treatment for non-insulin dependent  
 CC diabetes mellitus. The products can also be used for detection and  
 XX diagnosis.

SQ Sequence 312 AA;

Query Match 99.8%; Score 1616; DB 2; Length 312;  
 Beat Local Similarity 99.7%; Pred. No. 5.9e-165; 1; Mismatches 0; Indels 0; Gap 0;  
 Matches 311; Conservative 1;

Qy 1 MVGLKPSDVPPTMAYKFLGAGTAACTADLYTFPLDTAKVLQIOPENAQAVTARLVOYRG 60  
 Db 1 MVGLKPSDVPPTMAYKFLGAGTAACTADLYTFPLDTAKVLQIOPENAQAVTARLVOYRG 60  
 Qy 61 VLGTTILMVRTEGPSPYNGIVAGLQRQMSASIRGSPRSRKYSCMDAATRIBEGVGLWK 120  
 Db 61 VLGTTILMVRTEGPSPYNGIVAGLQRQMSASIRGSPRSRKYSCMDAATRIBEGVGLWK 120  
 Qy 121 LAGCTGAMAVTAOPTDVKVRFOASHINGPSPRSRKYSCMDAATRIBEGVGLWK 180  
 Db 121 LAGCTGAMAVTAOPTDVKVRFOASHINGPSPRSRKYSCMDAATRIBEGVGLWK 180  
 Qy 181 GTLPNIMRNATVCAEVTVTDILKEKLDYLTONPPCHEVSAGFCATVVASPVDV 240  
 Db 181 GTLPNIMRNATVCAEVTVTDILKEKLDYLTONPPCHEVSAGFCATVVASPVDV 240  
 Qy 241 VKTRYMSSPGQYFSLDCMIKVAQEGPTAFYKGFTPSFLRLGSNNVMFTYBOLKRA 300  
 Db 241 VKTRYMSSPGQYFSLDCMIKVAQEGPTAFYKGFTPSFLRLGSNNVMFTYBOLKRA 300  
 Qy 301 LMKVQMLRESPF 312  
 Db 301 LMKVQMLRESPF 312

RESULT 15

AAW81588

ID AAW81588 standard; protein; 403 AA.

XX AC AAW81588;

XX DT 09-FEB-1999 (first entry)

DE Protein encoded by human UCP3 gene reading frame 1.

XX Ucoupling protein 3; UCP3; thermogenesis; mammal; enhancer; drug;  
 KW protein catabolism; anti-obesity; inhibitor; muscle wasting; infection;  
 KW HIV; cancer; tumour cachexia; muscle disease; muscular dystrophy;  
 KW non-insulin dependent diabetes mellitus; diagnosis; human.

OS Homo sapiens.

XX Key Location/Qualifiers

PT 1. 403  
 PT /note= "the encoding reading frame has internal stop codons which are not indicated in this protein"

XX WO9845438-A1.

PN XX

XX PD 15-OCT-1998.

XX PR 08-APR-1998; 98WO-US005959.

XX PR 09-APR-1997; 97US-0043447P.  
 PR 12-MAY-1997; 97US-0046254P.  
 PR 15-JUL-1997; 97US-00892745.

XX PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

XX Lowell BB, Flier JS;

XX  
DR WPI: 1998-594483/50.  
DR N-PSDB; AAV71710.

XX  
PT New isolated uncoupling protein, UCP-3 - used to develop products for modulating thermogenesis in tissues, e.g. for treating obesity or muscle wasting caused by infection or cancer.

XX  
PS Disclosure; FIG 1A-C; 98pp; English.

CC Sequences AAW81588 to AAW81590 represent protein fragments encoded by the three reading frames of the human uncoupling protein 3 (UCP3) gene. The invention provides human and mouse UCP3 genes (AAV71710 and AAV71712), encoding UCP3 proteins (AAW81587 and AAW81595) respectively. A host cell transformed with a construct comprising the UCP3 nucleic acid can be used for the recombinant production of the protein. The UCP3 is involved in the regulation of thermogenesis in mammals. The nucleic acids (AAV71710 to AAV71712) can be used for identifying compounds which alter UCP3 activity. Enhancers of UCP3 can be used for enhancing protein catabolism in a mammal and can be used as anti-obesity drugs. Inhibitors of UCP3 can be used for inhibiting protein catabolism in a mammal such as inhibiting muscle wasting. They can be used for curtailing muscle wasting due to infection (e.g. HIV), cancer, tumour cachexia, muscle diseases (e.g. muscular dystrophy) or as a possible treatment for non-insulin dependent diabetes mellitus. The products can also be used for detection and diagnosis.

CC XX SQ Sequence 403 AA:

Query Match Similarity 99.4%; Score 1610; DB 2; Length 403;  
Best Local Similarity 99.4%; Pred. No. 3; 8e-164; 1; Mismatches 0; Indels 0;  
Matches 310; Conservative 1; Gaps 0;

QY	1	MVGLKISDVPPTMAVKPLFLGAGTACADLITPPLDTAKVRLQIQENQAVTARLIVQRG	60
Db	60	MVGLKISDVPPTMAVKPLFLGAGTACADLITPPLDTAKVRLQIQENQAVTARLIVQRG	119
QY	61	VLTGILTMVRATBGPSCPSPYNGAVAGLQRQMSAASIRGTVLQVTPKGADNSSLTRI	120
Db	120	VLTGILTMVRATBGPSCPSPYNGAVAGLQRQMSAASIRGTVLQVTPKGADNSSLTRI	179
QY	121	LAGCTTGAGAMATCAOPDIDVVKYRFOASIHGSPRSRSRDKYKSTMDAYRTIARBEVGRLWK	180
Db	180	LAGCTTGAGAMATCAOPDIDVVKYRFOASIHGSPRSRSRDKYKSTMDAYRTIARBEVGRLWK	239
QY	181	GILPNIMRNATVNCASVTTVILKEKULDMILTDIFCHVSARGAGFCITVVASPVDV	240
Db	240	GILPNIMRNATVNCASVTTVILKEKULDMILTDIFCHVSARGAGFCITVVASPVDV	299
QY	241	VKTRYMNSPPGQYFSPUDCMKVAQEGPTAFYKGTPSFIRLGSNNVMVTVYOLKRA	300
Db	300	VKTRYMNSPPGQYFSPUDCMKVAQEGPTAFYKGTPSFIRLGSNNVMVTVYOLKRA	359
QY	301	LMKVQMLRESPF 312	
Db	360	LMKVQMLRESPF 371	

Search completed: May 17, 2004, 11:51:55  
Job time : 61 secs



Db	301 LMKQVQIQLRESPF 312	Qy	301 LMK 303
<b>RESULT 2</b>			
G01858	uncoupling protein 1, mitochondrial - human	Db	296 LSK 298
N;Alternate name: UCP1			
C;Species: Homo sapiens (man)			
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 20-Jun-2000			
R;Bouillaud, F	submitted to the EMBL Data Library, June 1995		
A;Reference number: G08642			
A;Accession: G01858			
A;Molecule: translated from GB/EMBL/DDBJ			
A;Residues: 1-107 <BOU>			
A;Cross-references: EMBL:U28480; NID:9155218; PIDN:AAA85271.1; PID:9155219			
A;Accession: S8473			
A;Molecule type: DNA			
A;Residues: 1-10, P, 22-307 <BOU>			
A;Cross-references: EMBL:X51982; NID:937606; PIDN:CAA32214.1; PID:gi177311			
R;Cassard, A.M.; Bouillaud, P.; Mateei, M.G.; Hentz, B.; Raimbault, S.; Thomas, M.; Ricquier, D.			
J. Cell. Biochem. 43, 255-264, 1990			
A;Title: Human uncoupling protein gene: structure, comparison with rat gene, and assignment of chromosomal location			
A;Reference number: A45703; MUID:90338166; PMID:2380264			
A;Accession: S99141			
A;Molecule type: DNA			
A;Residues: 1-20, 'P', 22-108, 'SK', 111, 113-133, 'S', 135-197, 'I', 199-216, 'L', 218-307 <CAS>			
A;Cross-references: EMBL:X51982; NID:937606; PIDN:CAA32214.1			
R;Bouillaud, F.; Villarroya, F.; Hentz, B.; Raimbault, S.; Cassard, A.M.; Ricquier, D.			
Clin. Sci. 75, 21-27, 1988			
A;Title: Detection of brown adipose tissue uncoupling protein mRNA in adult patients by hybridization with cloned cDNA probes			
A;Reference number: A60793; MUID:89311701; PMID:3165741			
A;Accession: A60793			
A;Status: not compared with conceptual translation			
A;Molecule type: DNA			
A;Residues: 133-133, 'S', 135-196 <BOM>			
C;Comment: This protein is responsible for the generation of heat by brown fat.			
C;Genetics:			
A;Gene: GDB:UCPI; UCP			
A;Cross-references: GDB:128179; OMIM:113730			
A;Map position: 4q31-4q31			
A;Introns: 42/3; 109/1; 176/1; 210/1; 270/2			
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology			
C;Keywords: adipose tissue; duplication; mitochondrial; transmembrane protein			
F;10-103/Domain: ADP,ATP carrier protein repeat homology <ACPI>			
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>			
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP3>			
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP4>			
Query Match 56.2%; Score 910.5; DB 2; Length 307; Best Local Similarity 57.8%; Pred. No. 1.6e-75; Matches 175; Conservative 49; Mismatches 73; Indels 6; Gaps 3; Amino acid sequence alignment:			
Qy 1 MVGLKPSDVPPTMAYKFLGAGTAACFADLYPFPLDTAKVRLQIGENQAVQTLVQRG 60	Db 58 VLGTTTDLAKTEGPKLYSGLPAQKQRQISFASLRIGLKDLYPTQEFIT-SGEETPSLGSKI 116		
Qy 1 MVGTTTDLVPPTMWKGKPSAGVAAQCLADVTFPLTAKVRLQIGENQAVQTLVQRG 57	Db 1 MVGTTTDLVPPTMWKGKPSAGVAAQCLADVTFPLTAKVRLQIGENQAVQTLVQRG 57		
Qy 61 VLGTTTDLAKTEGPKLYSGLPAQKQRQISFASLRIGLKDLYPTQEFIT-SGEETPSLGSKI 120	Db 117 SAGLTGGGVAVFIGOPTEVVLRQASHRGLK--RYGTYNAVRIRIATTESTLSWK 174		
Qy 181 GTLPNITMRANVCATWVVTDLKEDLHLLTDPCHVSARGAGFCATVVASPVDF 240	Db 181 GTLPNITMRANVCATWVVTDLKEDLHLLTDPCHVSARGAGFCATVVASPVDF 240		
Db 175 GTPNLILRNVIINCTELVTDLMKGALVRLBLADDPVCHLSSLAGFCCTLSSPVDF 234	Db 175 GTPNLILRNVIINCTELVTDLMKGALVRLBLADDPVCHLSSLAGFCCTLSSPVDF 234		
Qy 241 VKTRYMSPPQYFESLDCMKVQAGEGPFAFYKFTPSFLRLGSMNNVMVFTYSQKRA 300	Db 241 VKTRYMSPPQYFESLDCMKVQAGEGPFAFYKFTPSFLRLGSMNNVMVFTYSQKRA 300		
Db 235 VCKTRFINSPPGQYASVENCAMTMTKEGPATAFFKGVPSPFLRLGSNDVIMVCFEKLGE 294	Db 235 VCKTRFINSPPGQYASVENCAMTMTKEGPATAFFKGVPSPFLRLGSNDVIMVCFEKLGE 294		
Qy 301 LMK 303	Db 295 LMK 297		
Db 295 LMK 297			
<b>RESULT 3</b>			
Qy 301 LMK 303	Qy 301 LMK 303	Qy 301 LMK 303	Qy 301 LMK 303
Db 296 LSK 298	Db 296 LSK 298	Db 296 LSK 298	Db 296 LSK 298
<b>RESULT 4</b>			
A26294	uncoupling protein - rat		
N;Alternate name: UCP			
C;Species: Rattus norvegicus (Norway rat)			
C;Date: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 18-Feb-2000			
R;Bouillaud, F.; Weissbach, J.; Ricquier, D.			
J. Biol. Chem. 261, 1487-1490, 1986			
A;Reference number: A26294; MUID:86111804; PMID:3753702			
A;Accession: A26294			
A;Molecule type: mRNA			
A;Residues: 1-307 <BOU>			
A;Cross-references: GR:MI11814; NID:9207556; PIDN:AAA19671.1; PID:9207557			
R;Ridley, R.G.; Patel, H.V.; Gerber, G.B.; Morton, R.C.; Freeman, K.B.			
Nucleic Acids Res. 14, 4025-4035, 1986			
A;Title: Complete nucleotide and derived amino acid sequence of cDNA encoding the mitoc			
Qy 236 VCKTRFINSPPGQYASVENCAMTMTKEGPATAFFKGVPSPFLRLGSNDVIMVCFEKLGE 295	Qy 236 VCKTRFINSPPGQYASVENCAMTMTKEGPATAFFKGVPSPFLRLGSNDVIMVCFEKLGE 295	Qy 236 VCKTRFINSPPGQYASVENCAMTMTKEGPATAFFKGVPSPFLRLGSNDVIMVCFEKLGE 295	Qy 236 VCKTRFINSPPGQYASVENCAMTMTKEGPATAFFKGVPSPFLRLGSNDVIMVCFEKLGE 295



F;110-202/Domain: ADP,ATP carrier Protein repeat homology <ACP2>  
F;209-296/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 53.9%; Score 873.5; DB 2; Length 307;  
Best Local Similarity 56.8%; Pred. No. 1.3e-72;  
Matches 172; Conservative 45; Mismatches 81; Indels 5; Gaps 2;

Qy 1 NNGLKEKSDVPPPTMAYRFLGAGTAACPADLVFPDQTAVKRLQIQENQENQAVQARLIVQYRG 60  
Db 1 NVNPNPTESEHPTWKGKIFSAQVAACLAIDITFPDQTAVKRLQIQEGQTSST--IRYKG 57

Qy 61 VLTGILTMVTEGGPSPPYNGVAGLQRQMSFASTIRIGLYNSVKQVTPKGADNSLITRI 120  
Db 58 VLTGILTMVTEGGPSPPYNGVAGLQRQMSFASTIRIGLYNSVKQVTPKGADNSLITRI 117

Qy 121 LAGCTTGAMAVTCAPTDVVKVRFOSHTHGPSRSRDKSCTMDAYTARBEGRGLWK 180  
Db 118 SAGLMWGGVAVPIQOPTEVVKRVLQOQSHAKIGK--RYTGTNAYRILATPESTLNWK 175

Qy 181 GTLPNIMNAVNCNEAVTVDILKEKLDHILTONPFCHEVSATGAGFCAVVASPVDV 240  
Db 176 GTTPNVLNVINCVELVTLMLKGALVNQNLADDPVCHLISLAWGFTTFLASPADV 235

Qy 241 VTKTRYMSPROQYFSPLDCMKVNAQEGPTAFYKGPPTSPFLRIGSMNWVMVFTVOLKRA 300  
Db 236 VTKTRFINSLPCQYPSVPSCAMTMLTKEGPTAFFKGFPVSPFLRILASWNVNMVCFFQLKKE 295

Qy 301 LMK 303  
Db 296 LSK 298

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RESULT 7

S03603 uncoupling protein - bovine (fragment)  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 20-Jun-2000  
C;Accession: S03603; S05075  
R;Casteilla, L.; Bouillaud, F.; Forrest, C.; Ricquier, D.  
Nucleic Acids Res. 17, 2131, 1989  
A;Title: Nucleotide sequence of a cDNA encoding bovine brown fat uncoupling protein. Hom  
A;Reference number: S03603; MUID:8318366; PMID:2928121  
A;Accession: S03603  
A;Molecule type: mRNA  
A;Cross-references: EMBL:X14064; NID:gi1495201; PIDN:CA13227.1; PID:gi1495202  
R;Ricquier, D.  
submitted to the EMBL Data Library, January 1989  
A;Reference number: S05075  
A;Accession: S05075  
A;Molecule type: mRNA  
A;Residues: 1-288 <CDS>  
A;Cross-references: EMBL:X14064  
A;Cross-references: EMBL:X14064  
C;Superfamily: ADP,ATP carrier protein repeat homology <ACP1>  
C;Keywords: duplication; mitochondrion; transmembrane protein  
F;1-87/Domain: ADP,ATP carrier protein repeat homology (fragment) <ACP2>  
F;92-184/Domain: ADP,ATP carrier protein repeat homology <ACP2>  
F;191-277/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 52.2%; Score 846; DB 2; Length 288;  
Best Local Similarity 58.9%; Pred. No. 4.1e-70; Matches 168; Conservative 46; Mismatches 61; Indels 10; Gaps 5;

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RESULT 9

T47570 uncoupling protein [imported] - Arabidopsis thaliana  
N;Alternate names: Protein F4B22-70  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Accession: TA7570; T52023  
R;Blocker, H.; Mewes, H.W.; Lemke, K.; Mayer, K.F.X.; Quétier, F.; Salanoubat, M.  
Submitted to the Protein Sequence Database, January 2000  
A;Reference number: 223016  
A;Accession: TA7570  
A;Status: Preliminary

Db 119 VVKVLQASHLHGK--PRYTGTNARYLIAITTEGTLWKGTPSPNLTNVINCTEV 175  
Qy 199 TYDLIKEKLDYHLITDPDNPFCHPSAFGAGFCATVVASPVDVVKTRYMSPPGQYFSPID 258  
Db 176 TYDLIKEKLDYHLITDPDNPFCHPSAFGAGFCATVVASPVDVVKTRYMSPPGQYFSPID 235  
Qy 259 CMIRONVAQSGPTATVKGFPSPFLRIGSMNWVMVFTVOLKRAIK 303  
Db 236 CAMMLTRIGPSAAPPKGFPVPSFLRIGSMNWVMVFCPERLQELMK 279

A;Molecule type: DNA  
A;Residues: 1-366 <BLO>  
A;Cross references: EMBL:AL132957  
A;Experimental source: cultivar Columbia; BAC clone F24B22  
R;Laioli, M.  
Submitted to the EMBL Data Library, August 1997  
A;Reference number: 225905  
A;Accession: T52023  
A;Status: preliminary; translated from GB/EMBL/DDJB  
A;Molecule type: mRNA  
A;Residues: 1-306 <LAN>  
A;Cross-references: EMBL:AJ001264; PIDN:CAA04638.1  
C;Genetics:  
A;Map position: 3  
A;Intcons: 26/3; 98/3; 125/1; 169/3; 202/3; 237/3; 263/3; 292/3  
A;Note: F24B22.70  
C;Superfamily: ADP, ATP carrier protein; ADP,ATP carrier protein repeat homology  
Query Match 42.1%; Score 682; DB 2; Length 306;  
Best Local Similarity 48.3%; Pred. No. 5; Se-55;  
Matches 146; Conservative 46; Mismatches 100; Indels 10; Gaps 6;  
Qy 1 MVGLKPSD--VRPTMAVKFLGAGTAACFADLVTPLDTAKVRLQIQQVTPKG 58  
Db 1 MVAAGKSDSLSPKTFAC---SAPAVGVGEVCTIPDTRKIQLO-KSALAGDVTPKV 55  
Qy 59 RGMVGTILTMWRNGPCSPYNGLVAGLQRQMSFASIRGLYSVTKQVTPKG-ADNSLT 117  
Db 56 RGLIGLGTGVTIAREEGRLSRSLWKGIVPGLRQCLFGRLGRIGMWPVKNLVKGDFGVDPVS 115  
Qy 118 TRIAGCTGAMAVTCQAQPTDVVKURFQASHINGPSRSRKYSGTMDAYRTTARECG 177  
Db 116 KITLAGLGTGAGLWVAMPDLVKYRQEGKLA-AGAPRYSQALNAYSTIVQEGRA 174  
Qy 178 LMKCTLPLNTMRNAIVNCABVUTTDILKEKULDHLLTONFPCHVSAFGAGFCATVVASP 237  
Db 175 LWLTLGLPNAVARNAINAAELASIDQVKETIKLKGFTINVUHLSGAGFAVCIGSP 234  
Qy 238 VDVVKTRYNNSSPGQYFSPIDCMKIVWQAGBGPFTAFYKGFPTSPFLRSWSVNVMFVTBOL 297  
Db 235 VDVVKSRMWD-SGAYKGTDIFCFVKTLSKSDGPMWFKGPIENFGRLGSWNVNIMFLTEQA 293  
Qy 298 KR 299  
Db 294 KK 295  
Db 294 KK 295

RESULT 10  
T52024  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 20-Oct-2000 #sequence\_revision 20-Oct-2000 #text\_change 03-Nov-2000  
C;Accession: T52024  
R;Maia, I.G.; Benedetti, C.E.; Leite, A.; Turcinelli, S.R.; Vercesi, A.E.; Arruda, P.  
FEBS Lett. 429, 403-406, 1998  
A;Title: Atump: an Arabidopsis gene encoding a plant uncoupling mitochondrial protein.  
A;Reference number: Z22968; MUID:962458; PMID:962458  
A;Accession: T52024  
A;Status: preliminary; translated from GB/EMBL/DDJB  
A;Molecule type: mRNA  
A;Residues: 1-306 <MAI>  
A;Cross-references: EMBL:AJ223983; PIDN:CAA11757.1  
C;Genetics:  
C;Keywords: brain; carrier protein; mitochondrion  
C;Superfamily: ADP, ATP carrier protein; ADP,ATP carrier protein repeat homology  
Query Match 32.3%; Score 524; DB 2; Length 325;  
Best Local Similarity 38.8%; Pred. No. 2; 1e-40;  
Matches 112; Conservative 60; Mismatches 101; Indels 16; Gaps 5;

Db 17 FLGAGTAACFADLVTPLDTAKVRLQIQQVTPKGVLTMRTEGCS 76  
Db 44 FVIGLASSIVAERGTFPPDLTKRLQGQSISDV-FKEIKRGMPHALPRIYREGIL 102  
Qy 77 PYNLGLVAGLQRQMSFASIRGLYSVTKQVTPKGADNSLTTRILAGCTGAMAVTCQ 136  
Db 103 LYSQIAPLAIROSYGTTKIGIYQSLKLFLVER-LEDETLIMICGVVSGVISIANP 161  
Qy 137 TDVKVKRQASHINGPSRSRKYSGTMDAYRTTARECGVJWKGTPNIMRNATCA 195  
Db 152 TDVLKIRQAQSL-----FQGSMGFSFDIYQGBTRGLWRGVPTGARAIWGV 213  
Qy 196 EVVYDIDKKEKLDYHLLDNFPCHFVSAFGAGFCATVVASPDVVKTRYMSPP---- 250  
Db 214 ELYVYDITKHLVSGMGDTIHFVFSFCGLAGLASNPDVVRTRMMNQRAIVCHV 273  
C;Description: may play a role in heat-requiring physiological events  
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology  
Query Match 41.5%; Score 673; DB 2; Length 306;  
Best local Similarity 48.0%; Pred. No. 3; e-54;  
Matches 145; Conservative 46; Mismatches 101; Indels 10; Gaps 6;  
Qy 1 MVGLKPSD--VRPTMAVKFLGAGTAACFADLVTPLDTAKVRLQIQQVTPKG 58  
Db 1 MVAGKSDSLSPKTFAC---SAPAVGVGEVCTIPDTRKIQLO-KSALAGDVTPKV 55  
Qy 59 RGVGTILTMWRNGPCSPYNGLVAGLQRQMSFASIRGLYSVTKQVTPKG-ADNSLT 117  
Db 56 RGLIGLGTGVTIAREEGRLSRSLWKGIVPGLRQCLFGRLGRIGMWPVKNLVKGDFGVDPVS 115  
Qy 118 TRIAGCTGAMAVTCQAQPTDVVKURFQASHINGPSRSRKYSGTMDAYRTTARECG 177  
Db 116 KKLAGLGTGALGIMVANPDLVKVRLQAEGLKA-AGAPRYSQALNAYSTIVQEGRA 174  
Qy 178 LMKCTLPLNTMRNAIVNCABVUTTDILKEKULDHLLTONFPCHVSAFGAGFCATVVASP 237  
Db 175 LWFVLGNVARDIAINAKELASIDQVKETIKLKGFTINVUHLSGAGFAVCIGSP 234  
Qy 238 VDVVKTRYNNSSPGQYFSPIDCMKIVWQAGBGPFTAFYKGFPTSPFLRSWSVNVMFVTBOL 297  
Db 235 VDVVKSRMWD-SGAYKGTDIFCFVKTLSKSDGPMWFKGPIENFGRLGSWNVNIMFLTEQA 293  
Qy 298 KR 299  
Db 294 KK 295  
Db 294 KK 295

RESULT 11  
T57553  
C;Species: Rattus norvegicus (Norway rat)  
C;Comment: This protein, a member of mitochondrial uncoupling protein family, has the role to uncouple oxidative phosphorylation in yeast.  
C;Genetics:  
A;Cross-references: GB:AF300424  
A;Experimental source: strain Male Wistar/ST  
A;Reference number: JCT553; MUID: 20549014; PMID:11095970  
A;Molecule type: mRNA  
A;Residues: 1-325 <MTZ>  
A;Accession: JCT553  
C;Keywords: brain; carrier protein; mitochondrion  
C;Superfamily: ADP, ATP carrier protein; ADP,ATP carrier protein repeat homology  
Query Match 32.3%; Score 524; DB 2; Length 325;  
Best Local Similarity 38.8%; Pred. No. 2; 1e-40;  
Matches 112; Conservative 60; Mismatches 101; Indels 16; Gaps 5;

Db 17 FLGAGTAACFADLVTPLDTAKVRLQIQQVTPKGVLTMRTEGCS 76  
Db 44 FVIGLASSIVAERGTFPPDLTKRLQGQSISDV-FKEIKRGMPHALPRIYREGIL 102  
Qy 77 PYNLGLVAGLQRQMSFASIRGLYSVTKQVTPKGADNSLTTRILAGCTGAMAVTCQ 136  
Db 103 LYSQIAPLAIROSYGTTKIGIYQSLKLFLVER-LEDETLIMICGVVSGVISIANP 161  
Qy 137 TDVKVKRQASHINGPSRSRKYSGTMDAYRTTARECGVJWKGTPNIMRNATCA 195  
Db 152 TDVLKIRQAQSL-----FQGSMGFSFDIYQGBTRGLWRGVPTGARAIWGV 213  
Qy 196 EVVYDIDKKEKLDYHLLDNFPCHFVSAFGAGFCATVVASPDVVKTRYMSPP---- 250  
Db 214 ELYVYDITKHLVSGMGDTIHFVFSFCGLAGLASNPDVVRTRMMNQRAIVCHV 273  
Qy 251 GOVSPSLCMIKAVQAEQPTAFLGKFTSPFLRGSWNVNMVFTYQKLR 299  
Db 274 DLVKGSTLGDILKMKWHEFFALYKGFWPNWLRLGPWNLIIFTYQKLR 322

RESULT 12  
T05577

uncoupling protein homolog F22K18\_230 - *Arabidopsis thaliana* (mouse-ear cress)  
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)  
 C;Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 04-Mar-2000  
 C;Accession: T05577  
 R;Bevan, M.; Wedler, H.; Wambutt, R.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.  
 A;Reference number: Z15419  
 A;Accession: T05577  
 A;Molecule type: DNA  
 A;Residues: 1-313 <REV>  
 A;Cross-references: EMBL:AL035356  
 A;Experimental source: cultivar Columbia; BAC clone F22K18  
 C;Genetics:  
 A;Map position: 4  
 A;Note: F22K18\_230  
 C;Superfamily: ADP,ATP carrier protein repeat homology  
 Best Local Similarity 30.9%; Score 500.5; DB 2; Length 313;  
 Matches 114; Conservative 51; Mismatches 123; Indels 23; Gaps 3;  
 QY 13 MAVK-FLGAGTACACFADLVTPLPDTAKVRLQIOPENQAQVATL-----  
 Db 1 NCVKTSVVEGGIGASVINGCSTPHPLDKVRLQHGEAPSTTVTLRPALEPNSSPAEFL 60  
 QY 56 -----VQYRGVLGTILMVRTGPGCSPYNGVLAGLQRQMSFASIRGLYMSVKQVTPKG 110  
 Db 61 ETTSSPKVGIGSLGNIVNVESEGAALFLSGVSATLKRQTLYSTTMGLYLVTKNTDPE 120  
 QY 111 ADNSSL-TTIALAGCTGCTGAMAVTCACQPTDWWVYKVRFOASHINGPSRSRDRKYSGTMAYRTIA 170  
 Db 121 SKKLNLRKIGAGLVLGVAGGIGAAGVGNPADVANVRMQADGRLL-PLAQARNAYGVGDARISMV 179  
 QY 171 RREGVGLWKGTLNPMNNAUNCAEVVYKTLKEKLDYHLLTNPCHVPSAGAGFC 230  
 Db 180 KQEGVLSLWRSLTINRAMTIAQDASYQFKEGIENQVMNDGILGTRAVASAAQFV 239  
 QY 231 ATVVASERDVVKTRYMNSPPGQYFSPLDCMVKONVAQEGPTAFYKGTSPRLRGLGSWNVM 290  
 Db 240 ASVASNPVDVVKTRVMMKVKAYDGAWDCAVKTVKAEGAMALYKGFPVTPCRQGPFTVVL 299  
 QY 291 FVTEQOLRKL 301  
 Db 300 FVTEQOLRKL 310

RESULT 13

H86224\_22 protein - *Arabidopsis thaliana*  
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)  
 C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 27-Nov-2001  
 C;Accession: H86224  
 R;Theologis, A.; Becker, J.R.; Palm, C.J.; Fedderspiel, N.A.; Kaul, S.; White, O.; Alonso, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creaby, T.H.; Dewar, K.; Hansen, N.P.; Hughes, B.; Huijar, L.  
 Nature 408, 816-820, 2000  
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luro, J.S.; Maiti, R.; Marzali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.; Venable, J.; Venter, A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.  
 A;Reference number: A86224; MUID:21016719; PMID:1130712  
 A;Status: Preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-305 <STO>  
 A;Cross-references: GB:AE005172; NID:95080790; PIDN:AAD39300.1; GSPDB:GN00139  
 C;Genetics:  
 A;Map position: 1  
 C;Superfamily: ADP,ATP carrier protein repeat homology  
 Query Match 29.5%; Score 478.5; DB 2; Length 305;

Best Local Similarity 37.0%; Pred. No. 2.9e-36;  
 Matches 108; Conservative 49; Mismatches 126; Indels 9; Gaps 4;

QY 11 PTMAYKFLGAGTACACFADLVTPLPDTAKVRLQIOPENQAQVATL-----  
 Db 11 PT-GTRILLASLSAVALAESTVFPDLTKTRMQLQGSGSAHNI---GAFFVSEIAR 65  
 A;Reference number: T05577  
 A;Accession: T05577  
 A;Molecule type: DNA  
 A;Residues: 1-313 <REV>  
 A;Cross-references: EMBL:AL035356  
 A;Experimental source: cultivar Columbia; BAC clone F22K18  
 C;Genetics:  
 A;Map position: 4  
 A;Note: F22K18\_230  
 C;Superfamily: ADP,ATP carrier protein repeat homology  
 Best Local Similarity 37.0%; Pred. No. 2.9e-36;  
 Matches 108; Conservative 49; Mismatches 126; Indels 9; Gaps 4;

QY 71 TEGPCSPNNGVAGLQRQMSFASIRGLYMSVKQVTPKGADNS--LITRILAGCTG 127  
 Db 66 KEVIGLYKGLSPALIRHLFYTPIRIYENLKLIVRSETTNNSESPLATKALVGGFSG 125  
 QY 128 AMAVTCAQPTDWWVKVRQFQASIHLCGSPRSRSRKYSGTMADYRTIAABEGVGLWKGTLPNM 187  
 Db 126 VIAQVVASPADLUVKVRMQADGRLLSQGLKPRYSPIEARTKILOSEGVGLWKGTLPNQ 185  
 QY 188 RNAIYNCAEVVYDILKEKLDYHLLTDPFCHVPSAFGFCATVUVASPVDPVWTRMN 247  
 Db 186 RAFLNMGEIACYDRAKHKVKKIADENFAHTIASLMSGLASTSISCPADVWTRMN 245  
 QY 248 SPPGQ-YFSPLDCMVKONVAQEGPTAFYKGTSPRLRGLGSWNVMFUTVQLK 298  
 Db 246 QGENAVYRNSYDCLVTKVPEGIRALWKSFEPPTWARGPWFOPFWVWSYER 297

RESULT 14

D84613 hypothetical protein At2g22500 [imported] - *Arabidopsis thaliana*  
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)  
 C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 16-Feb-2001  
 C;Accession: D84613  
 R;Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Talon, I.; euss, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.; Nature 402, 761-768, 1999  
 A;Title: Sequence and analysis of chromosome 2 of the Plant *Arabidopsis thaliana*.  
 A;Reference number: A84220; MUID:20083487; PMID:10617197  
 A;Accession: D84613  
 A;Gene: At2g22500  
 A;Map position: 2  
 C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology  
 Best Local Similarity 29.2%; Score 472.5; DB 2; Length 313;  
 Matches 114; Conservative 49; Mismatches 121; Indels 25; Gaps 6;

Query Match 29.2%; Score 472.5; DB 2; Length 313;  
 Best Local Similarity 36.9%; Pred. No. 1.1e-35; Indels 25; Gaps 6;  
 Matches 114; Conservative 49; Mismatches 121; Indels 25; Gaps 6;

QY 13 MAVK-FLGAGTACACFADLVTPLPDTAKVRLQIOPENQAQVATL-----  
 Db 1 MGLKGAEAGGIGASVINGCSTPHPLDKVRLQHGEAPSTTVTLRPALEPNSSPAEFL 60  
 QY 60 --GVGLMTMLVTRTECPSPYNGVLAGLQRQMSFASIRGLYMSVKQVTPKGADNSLT 117  
 Db 61 RVGVIGVGSRLIREGMRALFGSVSATLKRQTLYSTTMGLYDPIKEWTDPETKMPML 120  
 QY 118 TRILAGCTGCTGAMAVTCACQPTDWWVYKVRFOASHINGPSRSRDRKYSGTMADYRTIA 177  
 Db 121 KKIGAGAAGAAGAAGNPAVDVANVRMQADGRLL-PLAQARNAYGVGDARISMV 179  
 QY 178 LMKGTLNPMNNAUNCAEVVYDILKEKLDYHLLTDPFCHVPSAFGFCATVUVASPVDPVWTRMN 237  
 Db 180 LWGRSSLTINRAMLVTSQSLASQSYDSVETILEKGGLDGLGTHVSAASPAAGVVASNP 239  
 QY 238 VDVKVVKYMN-----SPPGQYFSPLDCMVKONVAQEGPTAFYKGTSPRLRGLGSWNVM 290  
 Db 240 VDVKVVKYMNVKVAGWAPP--YKGAWDCAVKTVKAGEMISLYKGFPVTPSRQGPFTVVL 299  
 QY 291 FVTEQOLRKL 301  
 Db 298 FVTEQOLRKL 306

RESULT 15

T15253

hypothetical protein K07B1.3 - *Caenorhabditis elegans*

C;Species:

*C. elegans*

C;Date:

20-Sep-1999 #sequence\_revision

20-Sep-1999

#text\_change

17-Mar-2000

C;Accession:

T15253

C;R;Pauley, A., Gattung, S.

R;Submitted to the EMBL Data library, May 1997

A;Description: The sequence of *C. elegans* cosmid K07B1.

A;Reference number: Z18317

A;Accession:

T15253

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-343 &lt;PAU&gt;

A;Cross-references: EMBL:AF003384; NTID:g2088817; PID:g2088821; PIDN:AAB54239.1; GSPDB:G1

A;Experimental source: strain Bristol N2; clone K07B1

A;Genetics:

A;Gene: CESP;K07B1.3

A;Map position: 5

A;Introns: 81/1; 131/3; 236/3; 279/2

C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 27.1%; Score 439; DB 2; Length 343;

Best local Similarity 33.3%; Pred. No. 1.5e-32;

Matches 98; Conservatism 56; Mismatches 118; Indels 22; Gaps 3;

QY 22 TAACFADLVTEPDPDIAKVLQIQCENQAVQTARIVQYRCVGLTILMWRTEGCPSPYNGL 81  
 ||||| :|:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 49 TAAALVAETTYPLDITKIRLQIARNKFKPGGMWQ----VYDIDIRREGAMALWGV 102  
 |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 Db 82 VAGLQORMSFASISTRIGLYNSVKOVYTPKGADS-SLTTRILASCTGTGAMAVTCQPTDW 140  
 |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 Db 103 APAITRHYITYTGIRKMGAYEQRILLTFNKEVEKSFRPLWKSMLCGAPSGLIAQQFAASPTDLV 162  
 |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 QY 141 KVRQOASITHLGPSRSDRKYSCTMDAYRTIARBEVGRLWKGTLLENIMENAINVCAEVY 200  
 |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 Db 163 KVQDMQMEGARRLOKOPRLYTGTATCFSRLYRTDCCFGWMGNPNCORALLNMADIY 222  
 |||:|||:|||:|||:|||:|||:|||:|||:  
 QY 201 DILKEKLUDYHLLTDNFCHFFVSARGAGECATVVASPVVVKRYM----- 246  
 |||:|||:|||:|||:|||:|||:|||:|||:  
 Db 223 DSVKHGLIDNFEICDNMLTHAVASACAGLAAIVSLPSVWKIRMMQIRHELDARKMK 282  
 |||:|||:|||:|||:|||:|||:|||:  
 QY 247 -NSPRGQOVESPLDNEWIKWVQEGPTAFYKGPTRSPFLRGWSWVVMFVTVBOLKR 299  
 |||:|||:|||:|||:|||:|||:|||:  
 Db 283 KNTHDVLDLYKGVVDCVYKIKRNKEGFPFLPSLYKGFLPSLYMMAFWSLTFWVSYEBIRK 336

Search completed: May 17, 2004, 11:53:55  
Job time : 21 secs



Db 177 GTWPNTIRNAVNCAEWNTIDIKEKUDSHLFTDNPPCHVSAGFCAGFCATIVASPV 236  
 Qy 241 VKTRYTNSPCCQYFSPFLDCMKVMAQEGPAPAFYKPTPSLRLGSWNVWVFTYEQKRA 300  
 Db 237 VKTRYNAPPGRYSPHLCHMLKOMVAQEGPTAFYKGMPSFLRLGAWNVMWVFTYEQKRA 296  
 Qy 301 ---LMKVQMLRESP 312  
 Db 297 LESKUMKVQMLRESP 312

RESULT 2

Q9ER16 PRELIMINARY; PRT; 299 AA.  
 ID Q9ER16  
 AC Q9ER16;  
 DT 01-MAR-2001 (TREMBrel. 16, Created)  
 DT 01-MAR-2001 (TREMBrel. 16, Last sequence update)  
 DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)

DBQ Uncoupling protein 3 (Fragment).  
 OS Photopus sungsorae (Striped hairy-footed hamster) (Djungarian hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OX Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Photopus  
 OX NCBI\_TaxID=10044;  
 RN [1]

RC SEQUENCE FROM N.A.

RA TISSUE=Brown adipose tissue;  
 RA von Praun C., Burkert M., Gessner M., Klingenspor M.;  
 RT "Tissue-specific expression and cold-induced mRNA levels of uncoupling  
 proteins in the Djungarian hamster";  
 RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.  
 CC -I SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.  
 DR EMBL: AF271265 AAC39851; -;  
 DR GO; GO:0016021; C:mitochondrial inner membrane; IEA.  
 DR GO; GO:005739; C:mitochondrion; IEA.  
 DR GO; GO:005488; P:binding; IEA.  
 DR GO; GO:0006839; P:mitochondrial transport; IEA.  
 DR GO; GO:006810; P:transport; IEA.  
 DR InterPro: IPR01993; Mitoch\_carrier.  
 DR InterPro: IPR002067; Mit\_carrier.  
 DR IntexPro: IPRO02030; Mit\_uncoupling.  
 DR Pfam: PF00153; mito\_carr\_3.  
 DR PRINTS: PR00784; MTUNCOUPLING.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 DR Membrane; Transmembrane; Transport.  
 FT NON\_TER 299 299  
 SQ SEQUENCE 299 AA; 32784 MW; AB5C947BADDCA9A0 CRC64;

Query Match 72 %; Score 178; DB 6; Length 310;  
 Best Local Similarity 72.6%; Pred. No. 3.4e-10;  
 Matches 228; Conservative 34; Mismatches 46; Indels 6; Gaps 3;

Matches 228; Conservative 34; Mismatches 46; Indels 6; Gaps 3;

Qy 1 MVGLKPSDVPMPTMVKFLGACTACPAFLDVTTPDTAKVRLQIOQENAOV-QTARVQV 58  
 Db 1 MVGRKPTDPPTATVKFLGAGTAATDADLTTPDTAKVRLQIOQENAOV-QTARVQV 60

Qy 59 RGVVLGTTMWRTEGGSPNGLVAGLORNSFAISIRGKIDSQVQVTFKGADNSLITR 118  
 Db 61 RGVMGILTMTVKTEPGSLVNGLVLQIQLQMSFASVRLGDSVQFF-KGAERASIGS 119

Qy 119 RIAAGCTTGAMAVTCQPTDVKVRQFASIRGKIDSQVQVTFKGADNSLITR 178

Db 120 RIAAGCTTGALAVAAQDQVQQAQAGGSS--RRQGTVDAIKTARESGRL 176

Qy 179 WKGTLRNMIRNAVNCAEVVTDIKEKUDSHLFTDNPPCHVSAGFCAGFCATIVASPV 238

Db 177 WRGTSNTIARNAVNCAEVVTDIKEKUDSHLFTDNPPCHVSAGFCAGFCATIVASPV 236

Qy 239 DVKTRYTNSPCCQYFSPFLDCMKVMAQEGPTAFYKGMPSFLRLGAWNVMWVFTYEQK 298

Db 237 DVKTRYTNSPCCQYFSPFLDCMKVMAQEGPTAFYKGMPSFLRLGAWNVMWVFTYEQK 296

Qy 299 RALMKVQMLRESP 312

Db 297 RALMAARTSREVSP 310

RESULT 4

Q7ZKX1 PRELIMINARY; PRT; 307 AA.  
 ID Q7ZKX1  
 AC Q7ZKX1;  
 DT 01-JUN-2003 (TREMBrel. 24, Created)  
 DT 01-JUN-2003 (TREMBrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)

DBQ Hypothetical protein.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OC NCBI\_TaxID=8355;  
 RN [1]

RC SEQUENCE FROM N.A.

TISSUE=Embryo;

Db 237 VKTRYNAPPGRYSPHLCHMLKOMVAQEGPTAFYKGMPSFLRLGAWNVMWVFTYEQKRA 296  
 Qy 301 L 301  
 Db 297 L 297

Qy 181 GLPNLNGNATNCACVUTYDILKEKUDSHLFTDNPPCHVSAGFCAGFCATIVASPV 240  
 Db 177 GTWPNTIRNAVNCAEVVTDIKEKUDSHLFTDNPPCHVSAGFCAGFCATIVASPV 236

Qy 241 VKTRYTNSPCCQYFSPFLDCMKVMAQEGPTAFYKGMPSFLRLGAWNVMWVFTYEQKRA 300

RA Klein S.; Strausberg R.;  
 RL Submitted [JAN-2003] to the EMBL/GenBank/DDBJ databases.  
 DR BMBL; BC044682; ARH46682.1; -.  
 DR GO; GO:001020; C:mitochondrane; IEA.  
 DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 DR GO; GO:0005488; F:binding; IEA.  
 DR GO; GO:0003824; F:catalytic activity; IEA.  
 DR GO; GO:0006333; F:fatty acid biosynthesis; IEA.  
 DR GO; GO:0008939; P:mitochondrial transporth; IEA.  
 DR GO; GO:0006413; P:translational initiation; IEA.  
 DR GO; GO:0008810; P:transport; IEA.  
 DR InterPro; IPR000794; Ketoacyl synth.  
 DR InterPro; IPR001993; Mitoch carrier.  
 DR InterPro; IPR002030; Mit uncoupling.  
 DR PRAM; PF00153; mito\_carr; 3.  
 DR PROSITE; PS00784; MTUNCOUPLING.  
 DR PROSITE; PS00606; B\_KETOACYL\_SYNTHASE; 1.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 DR KW Hypothetical protein.  
 SQ SEQUENCE 307 AA; 33446 MW; 903BIF25ASD1F86 CRC64;  
 Query Match 72.4%; Score 1173.5; DB 13; Length 307;  
 Best Local Similarity 72.1%; Pred. No. 8.8e-102;  
 Matches 225; Conservative 35; Mismatches 47; Indels 5; Gaps 3;  
 QY 1 MVGILKPSVPPTMVKFAGTACFADLVTFLDTAKVRLQGENAVQVTLVQRG 60  
 Db 1 MVGILKPSVPPTMVKFAGTACFADLVTFLDTAKVRLQGENAVQVTLVQRG 59  
 QY 61 VLGILTLMVRTECPSPCSPNGLVAGLQRQMSFASIRIGLYDSVKQVTPKGANSLSITRI 120  
 Db 60 VGGTISTVAKMSEPKSKLNGLAAGLQRQMSFASIRIGLYDSVKQVTPKGANSLSITRI 118  
 QY 121 LAGCTTGAMAVTCAOPTDVVKRPOASITHLGPSSDRKYSRKGTVMDAYTARERGVGJMK 180  
 Db 119 AGCTTGAMAVTCAOPTDVVKRPOASITHLGPSSDRKYSRKGTVMDAYTARERGVGJMK 175  
 QY 181 KGTLPNIRNATVCAEVVTTDYLKEKLDYHLLTDNPFCHPVSAGFAGFCATVASPVD 240  
 Db 176 GTVNTENNAVTCETLYTDYLKOSILKANIWTDNLPCPHFSAFGFCTTVIASPV 235  
 QY 241 VKTRYMSPPGQFSPSLCMKVAQSGPTAFTKGFTPSFLRGWSWNTVMFTYEQLRA 300  
 Db 236 VTKTRYMSAKGQTSALNCALTMFRKEGRFAYKGEMPSFLRLGSWNVUMFTYEQLRA 295  
 QY 301 ALMKVQMLRESP 312  
 Db 296 MMSAQRSKAPF 307  
 DR RESULT 5  
 ID Q90X50 PRELIMINARY; PRT; 307 AA.  
 AC Q90X50:  
 DT 01-DEC-2001 (TREMBREL. 19, Created)  
 DT 01-DEC-2001 (TREMBREL. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBREL. 25, Last annotation update)  
 DE Uncoupling protein UCP.  
 OS *Melaeverta gallipavo* (Common turkey).  
 OC Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosuria; Aves; Neognathae; Galliformes; Phasianidae; Melagris.  
 OX NCBI\_TaxID:9103;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Skeletal muscle;  
 RA Brock-Clover C.M., Poch S.M., Richards M.P.;  
 RL Submitted (Oct-2001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL: AF430811; AAL28138.1; -.  
 DR GO; GO:001020; C:membrane; IEA.  
 DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 DR GO; GO:0005488; F:binding; IEA.  
 DR GO; GO:0008824; F:catalytic activity; IEA.

DR GO; GO:0003743; F:translation initiation factor activity; IEA.  
 DR GO; GO:0006333; P:fatty acid biosynthesis; IEA.  
 DR GO; GO:0008939; P:mitochondrial transporth; IEA.  
 DR GO; GO:0006413; P:translational initiation; IEA.  
 DR GO; GO:0008810; P:transport; IEA.  
 DR InterPro; IPR000794; Ketoacyl synth.  
 DR InterPro; IPR001993; Mitoch carrier.  
 DR InterPro; IPR002030; Mit uncoupling.  
 DR InterPro; IPR001950; TIF\_SU1.  
 DR PRAM; PF00153; mito\_carr; 3.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 DR KW Hypothetical protein.  
 SQ SEQUENCE 307 AA; 33148 MW; 256566D66B8B2ECCC CRC64;  
 Query Match 72.0%; Score 1166.5; DB 13; Length 307;  
 Best Local Similarity 72.1%; Pred. No. 4e-101; Mismatches 42; Indels 7; Gaps 3;  
 Matches 225; Conservative 38; Mismatches 42; Indels 7; Gaps 3;  
 QY 1 MVGILKPSVPPTMVKFAGTACFADLVTFLDTAKVRLQGENAVQVTLVQRG 60  
 Db 1 MVGILKPSVPPTMVKFAGTACFADLVTFLDTAKVRLQGENAVQVTLVQRG 59  
 QY 61 VLGILTLMVRTECPSPCSPNGLVAGLQRQMSFASIRIGLYDSVKQVTPKGANSLSITRI 120  
 Db 61 VLGILTLMVRTECPSPCSPNGLVAGLQRQMSFASIRIGLYDSVKQVTPKGANSLSITRI 118  
 QY 121 LAGCTTGAMAVTCAOPTDVVKRPOASITHLGPSSDRKYSRKGTVMDAYTARERGVGJMK 180  
 Db 121 LAGCTTGAMAVTCAOPTDVVKRPOASITHLGPSSDRKYSRKGTVMDAYTARERGVGJMK 175  
 QY 180 KGTLPNIRNATVCAEVVTTDYLKEKLDYHLLTDNPFCHPVSAGFAGFCATVASPVD 239  
 Db 178 KGTLPNIRNATVCAEVVTTDYLKEKLDYHLLTDNPFCHPVSAGFAGFCATVASPVD 237  
 QY 240 VKTRYMSPPGQFSPSLCMKVAQSGPTAFTKGFTPSFLRGWSWNTVMFTYEQLRA 299  
 Db 238 VTKTRYMSAKGQTSALNCALTMFRKEGRFAYKGEMPSFLRLGSWNVUMFTYEQLRA 297  
 QY 300 ALMKVQMLRESP 311  
 Db 298 VWM---LARSAP 306  
 DR RESULT 6  
 ID Q9R246 PRELIMINARY; PRT; 309 AA.  
 AC Q9R246:  
 DT 01-MAY-2000 (TREMBREL. 13, Created)  
 DT 01-MAY-2000 (TREMBREL. 13, Last sequence update)  
 DT 01-OCT-2003 (TREMBREL. 25, Last annotation update)  
 DE Uncoupling protein 2.  
 GN UCP2.  
 OS *Mus musculus* (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID:10909;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CASTE1;  
 RK MEDLINE=9268912; PubMed=10337618;  
 RA York B., Trinett A.A., Monteiro M.P., Barry S.J., Warden C.H.,  
 RA Naggett J.M., Maddatu T.P., West D.B.;  
 RT "Gene environment interaction: a significant diet-dependent obesity locus demonstrated in a congenic segment on mouse chromosome 7.";  
 RT Mam. Genome 10:457-462 (1999).  
 CC --SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.  
 DR EMBL: AP111999; RAD1199.1; -.  
 DR EMBL: MC110354; RAD1199.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 DR GO; GO:0005488; F:binding; IEA.  
 DR GO; GO:0006839; :mitochondrial transport; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR01993; Mitoch\_carrier.  
 DR InterPro; IPR002030; Mit\_uncoupling.  
 DR Pfam; PF00153; mito\_carr; 3.  
 DR PRINTS; PR0074; MITUCOUPLING.  
 DR PROSITE; PS0215; MITOCH\_CARRIER; 3.  
 DR Membrane; Transmembrane; Transport.  
 SQ SEQUENCE 309 AA; 33313 MW; B03794EB99810FO CRC64;  
 Query Match 71.8%; Score 1163.5; DB 11; Length 309;  
 Best Local Similarity 72.8%; Pred. No. 7.7e-101;  
 Matches 228; Conservative 31; Mismatches 49; Indels 5; Gaps 3;  
 QY 1 MVGLKESDVPPTMVKRFACTADLTVPLDTAKVRQIQENQA-VOTARIUVOYR 59  
 1 MVGKFATDVPPATVKEFAGTAACTADLITFPFLDTAKVRQIQLQEGSQGLVRTASAQR 60  
 QY 60 VLTGTILTMVTEGCPSPYNGIVAGQORMSPASISTRIGLDSVSKVQYTPKGADNSLTT 119  
 61 VLTGTILTMVTEGCPSPYNGIVAGQORMSPASISTRIGLDSVSKVQYTPKGADNSLTT 119  
 Db QY 120 RGTLPITMIRNIAVNCBVTIDLEKULDPHLLNPCHFVSAFGAGRAVWASPVD 179  
 120 LLAGSTTGALAVAVAGPTDVVKVRQDQARAG--GGRYVSTVEAKTIREGIRLW 176  
 Db QY 180 RGTLPITMIRNIAVNCBVTIDLEKULDPHLLNPCHFVSAFGAGRAVWASPVD 239  
 177 KGTSPNVARNIAVNCBVLTVTDLKLQTKNLMTDLPCHTSAFGAGRCITVIASPV 236  
 Qy 240 VKTRTRNNSPQQYFSPLDCMKWVQEGPFAFKGKPTSPSLRSLASWNVNMFVTEQLR 299  
 237 VTKTRTRNNSPQQYFSPLDCMKWVQEGPFAFKGKPTSPSLRSLASWNVNMFVTEQLR 296  
 Db QY 300 ALMKVOMLRESPP 312  
 297 ALMAACOSREAPP 309  
 Db QY 307 AA; 33130 MW; 33AC1CD6FC19CD CRC64;  
 Query Match 71.8%; Score 1162.5; DB 13; Length 307;  
 Best Local Similarity 71.8%; Pred. No. 9.5e-101;  
 Matches 224; Conservative 38; Mismatches 43; Indels 7; Gaps 3;  
 QY 1 MVGLKESDVPPTMVKRFACTADLTVPLDTAKVRQIQENQA-VOTARIUVOYR 60  
 1 MVGLKESDVPPTMVKRFACTADLTVPLDTAKVRQIQENQA-VOTARIUVOYR 60  
 Qy 61 VLTGTILTMVTEGCPSPYNGIVAGQORMSPASISTRIGLDSVSKVQYTPKGADNSLTT 120  
 Db QY 61 VLTGTILTMVTEGCPSPYNGIVAGQORMSPASISTRIGLDSVSKVQYTPKGADNSLTT 120  
 Db QY 121 LAGCTTGAMVTCOPTDVVKVRQDQARAG--LGALPESNRYSGTVDVARTIAREGVGLW 179  
 121 LAGCTTGAMVTCOPTDVVKVRQDQARAG--LGALPESNRYSGTVDVARTIAREGVGLW 177  
 Db QY 180 RGTLPITMIRNIAVNCBVTIDLEKULDPHLLNPCHFVSAFGAGRAVWASPVD 239  
 178 RGTLPITMIRNIAVNCBVTIDLEKULDPHLLNPCHFVSAFGAGRAVWASPVD 237  
 Db QY 240 VKTRTRNNSPQQYFSPLDCMKWVQEGPFAFKGKPTSPSLRSLASWNVNMFVTEQLR 299  
 238 VKTRTRNNSPQQYFSPLDCMKWVQEGPFAFKGKPTSPSLRSLASWNVNMFVTEQLR 297  
 Qy 300 ALMKVOMLRESPP 311  
 298 VTM---IARSAP 306  
 Db QY 306 AA; 33130 MW; 33AC1CD6FC19CD CRC64;  
 RESULT 7  
 Q9DDT7 PRELIMINARY; PRT; 307 AA.  
 ID Q9DDT7; AC 09DDT7;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Mitochondrial uncoupling protein.  
 GN UCP.  
 OS Galus gallus (Chicken).  
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Gallus.  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxId=9031;  
 RN [1]  
 SEQUENCE FROM N A.  
 TISSUE=Muscle;  
 RX MEDLINE=21092869; PubMed=1171038;  
 RA Rimbault S., Dridi S., Denjean F., Lachuer J., Couplan E.,  
 RA Bouillaud F., Bordas A., Duchamp C., Taouis M., Roquier D.;  
 RT "An uncoupling protein homolog putatively involved in facultative muscle thermogenesis in birds.";  
 RL Biochem., J. 353:441-444(2001).  
 RN [2]  
 SEQUENCE FROM N A.  
 RC TISSUE=Blood;  
 RA Zhao J., Wang Q., Meng H., Gu Z., Li H.;  
 RT "Cloning and Sequencing of Uncoupling Protein Gene in Chicken.";  
 Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.  
 CC -SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.  
 EMBL; AF287144; AAG48942.1; -. .  
 DR EMBL; AR433170; AAL35325.2; -. .  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.  
 DR GO; GO:0006739; C:mitochondrion; IEA.  
 DR GO; GO:0005488; F:binding; IEA.  
 DR GO; GO:0003824; F:catalytic activity; IEA.  
 DR GO; GO:0003743; F:translation initiation factor activity; IEA.  
 DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.  
 DR GO; GO:0006839; P:mitochondrial transport; IEA.  
 DR GO; GO:0006413; P:translational initiation; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR001993; Mitoacyl synth.  
 DR InterPro; IPR001993; Mitoch\_carr.  
 DR InterPro; IPR002067; Mit\_carr.  
 DR InterPro; IPR002030; Mit uncoupling.  
 DR PROSITE; PS00606; B\_KETOCYL\_SYNTHASE; 1.  
 DR PROSITE; PS0215; MITOCH\_CARRIER; 3.  
 DR PROSITE; PS01118; SUL1; 1.  
 DR Membrane; Transmembrane; Transport.  
 SQ SEQUENCE 307 AA; 33130 MW; 33AC1CD6FC19CD CRC64;  
 Query Match 71.8%; Score 1162.5; DB 13; Length 307;  
 Best Local Similarity 71.8%; Pred. No. 9.5e-101;  
 Matches 224; Conservative 38; Mismatches 43; Indels 7; Gaps 3;  
 QY 1 MVGLKESDVPPTMVKRFACTADLTVPLDTAKVRQIQENQA-VOTARIUVOYR 60  
 1 MVGLKESDVPPTMVKRFACTADLTVPLDTAKVRQIQENQA-VOTARIUVOYR 60  
 Qy 61 VLTGTILTMVTEGCPSPYNGIVAGQORMSPASISTRIGLDSVSKVQYTPKGADNSLTT 120  
 Db QY 61 VLTGTILTMVTEGCPSPYNGIVAGQORMSPASISTRIGLDSVSKVQYTPKGADNSLTT 120  
 Db QY 121 LAGCTTGAMVTCOPTDVVKVRQDQARAG--LGALPESNRYSGTVDVARTIAREGVGLW 179  
 121 LAGCTTGAMVTCOPTDVVKVRQDQARAG--LGALPESNRYSGTVDVARTIAREGVGLW 177  
 Db QY 180 RGTLPITMIRNIAVNCBVTIDLEKULDPHLLNPCHFVSAFGAGRAVWASPVD 239  
 178 RGTLPITMIRNIAVNCBVTIDLEKULDPHLLNPCHFVSAFGAGRAVWASPVD 237  
 Db QY 240 VKTRTRNNSPQQYFSPLDCMKWVQEGPFAFKGKPTSPSLRSLASWNVNMFVTEQLR 299  
 238 VKTRTRNNSPQQYFSPLDCMKWVQEGPFAFKGKPTSPSLRSLASWNVNMFVTEQLR 297  
 Qy 300 ALMKVOMLRESPP 311  
 298 VTM---IARSAP 306  
 Db QY 306 AA; 33130 MW; 33AC1CD6FC19CD CRC64;



DR GO; GO:0066839; P:mitochondrial transport; IEA.  
 DR GO; GO:006810; P:transport; IEA.  
 DR InterPro; IPR01993; Mito\_carrier.  
 DR InterPro; IPR02000; Mit\_uncoupling.  
 DR Pfam; PF00153; mito\_carr; 3.  
 DR PROSITE; PS00784; MITUNCOUPLING.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 KW Membrane; Transmembrane; Transport.  
 SEQUENCE 309 AA; 33359 MW; 9D9C4C1B169F2771 CRC64;

Query Match 71.5%; Score 1158.5; DB 11; Length 309;  
 Best Local Similarity 72.2%; Pred. No. 2.3e-100; Mismatches 49; Indels 5; Gaps 3;  
 Matches 226; Conservative 33; Mismatches 49; Indels 5; Gaps 3;

Qy 1 MVGLKESDVPTMAVEKAGTAACFAFDLVPFLDTAKVRQIQLQIGENQAV-QTARLUVOYR 59  
 Db 1 MVGFKATDVPIPATVKFAGTAACIADLTFPFLDTAKVRQIQLQIGENQAV-QTARLUVOYR 60

Qy 120 ILAGCTGAMAVTCQOPTDVKURFOASHIG-PGSRSDRKYSGTMAYRTARECGVRLN 179  
 Db 120 ILAGSTTGALAVAVAGOPTDVKURFOASHIG-PGSRSDRKYSGTMAYRTARECGVRLN 176  
 Db 61 GTVLGTTLMVTEGRPSLYNGEVAGLQRQMSFASVRLGVYKOFYT-KOSEHAGIGSR 119

Qy 180 KGTLPNTMNRNAIVNCABVUTVDILKEKULDYHLLTNFPCFVSAFGAGFCATVAVASPVD 239  
 Db 177 KGTSPNVARNAIVNCABLVTDLIKOTKLKANLMDLPCKFTSARGAGFTCIVASPVD 236

Qy 240 VKTRTNSPSPGQYFSPLCDMKMVQAEPPAFYKOPTPSLTSRSLSWNNVVFYEQQLKR 299  
 Db 237 VTKTRTNSALGQHSGHCAUTMLRKEGPRFYKGPMPSFLRGLGSWNWVMPVYBQLR 296

Qy 300 ALMKVQMLRESPP 312  
 Db 297 ALMAAIVESRAPP 309

RESULT 11

ID Q98T90 PRELIMINARY; PRT; 304 AA.  
 AC 098T90;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DB Mitochondrial uncoupling protein UCP.  
 OS Bupetomena macrotria (swallow-tailed hummingbird).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archobacteria; Aves; Neognathae; Trochiliformes; Trochilidae;  
 OC Bupetomena.  
 OX NCBI\_TAXID=153633;  
 RN [1] SEQUENCE FROM N.A.

RA Vianna C.R., Hogen T., Zhang C.-Y., Bachman E., Bass O., Gereben B.,  
 RA Morisot A.S., Lowell B.B., Bicudo J.S.P.W., Bianco A.C.,  
 RT "Cloning and functional characterization of an uncoupling protein  
 homolog in hummingbirds."  
 RL Physiol. Genomics (online) 0: 0 (2001).

C1 - SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

DR EMBL: AF257279; AACU6829\_1; -.  
 DR GO; GO:015021; C:integral to membrane; IEA.  
 DR GO; GO:005743; C:mitochondrial inner membrane; IEA.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 DR GO; GO:005488; F:binding; IEA.  
 DR GO; GO:005488; F:binding; IEA.  
 DR GO; GO:003824; F:catalytic activity; IEA.  
 DR GO; GO:003743; P:translocation initiation factor activity; IEA.  
 DR GO; GO:006633; P:fatty acid biosynthesis; IEA.  
 DR GO; GO:006839; P:mitochondrial transport; IEA.  
 DR GO; GO:005613; P:translational initiation; IEA.  
 DR InterPro; IPR00794; Ketoacyl\_Synth.

Query Match 70.4%; Score 1141; DB 13; Length 304;  
 Best Local Similarity 71.7%; Pred. No. 9.8e-99; Mismatches 46; Indels 2; Gaps 1;  
 Matches 215; Conservative 37; Mismatches 46; Indels 2; Gaps 1;

Qy 1 MVGLKESDVPTMAVEKAGTAACFAFDLVPFLDTAKVRQIQLQIGENQAV-QTARLUVOYR 59  
 Db 1 MVALKSQEMPTAAIKFPSAGTAGPDLCTFPFLDTAKVRQIQLQIGENQAV-QTARLUVOYR 60

Qy 61 VLGTLTVMVTEGCSPYNGEVAGLQRQMSFASVRLGVYKOFYT-KOSEHAGIGSR 120  
 Db 61 VLGTLTVMVTEGRPSLYNGEVAGLQRQMSFASVRLGVYKOFYT-KOSEHAGIGSR 119

Qy 121 IAGCTGAMAVTCQOPTDVKURFOASHIG-PGSRSDRKYSGTMAYRTARECGVRLN 180  
 Db 121 IAGSTTGALAVAVAGOPTDVKURFOASHIG-PGSRSDRKYSGTMAYRTARECGVRLN 178  
 Db 179 GTLPNTMNRNAIVNCABVUTVDILKEKULDYHLLTNFPCFVSAFGAGFCATVAVASPVD 240  
 Db 179 GTLPNTMNRNAIVNCABLVTDLIKOTKLKANLMDLPCKFTSARGAGFTCIVASPVD 238

Qy 241 VKTRTNSPSPGQYFSPLCDMKMVQAEPPAFYKOPTPSLTSRSLSWNNVVFYEQQLKR 300  
 Db 239 VKTRTNSALGQHSGHCAUTMLRKEGPRFYKGPMPSFLRGLGSWNWVMPVYBQLR 298

RESULT 12

ID Q7ZVP4 PRELIMINARY; PRT; 309 AA.  
 AC Q7ZVP4;  
 DT 01-JUN-2003 (TREMBLrel. 24, Created)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DB Hypothetical protein.  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Bupetomena; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TAXID=7955;  
 RN [1] SEQUENCE FROM N.A.  
 RP TISSUE=Body;  
 RA Straubberg R.;  
 RL Submitted (JAN-2-2003) to the EMBL/GenBank/DDBJ databases.  
 DR Submitted (JAN-2-2003) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; BC05464; AAHK5464\_1; -.  
 DR GO; GO:001620; C:membrane; IEA.  
 DR GO; GO:005743; C:mitochondrial inner membrane; IEA.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 DR GO; GO:005488; F:binding; IEA.  
 DR GO; GO:006839; P:mitochondrial transport; IEA.  
 DR GO; GO:006810; P:transport; IEA.  
 DR InterPro; IPR01993; Mito\_carrier.  
 DR InterPro; IPR002030; Mit\_uncoupling.  
 DR Pfam; PF00153; mito\_carr; 3.  
 DR PRINTS; PRO0784; MITUNCOPLING.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 KW Hypothetical protein.  
 SEQUENCE 309 AA; 33766 MW; C10F74C1FECB929 CRC64;

Query Match 69.6%; Score 1127.5; DB 13; Length 309;  
 Best Local Similarity 72.2%; Pred. No. 1.9e-97; Mismatches 48; Indels 3; Gaps 2;  
 Matches 218; Conservative 33; Mismatches 48; Indels 3; Gaps 2;

Qy 1 MVGLKESDVPTMAVEKAGTAACFAFDLVPFLDTAKVRQIQLQIGENQAV-QTARLUVOYR 60



RA Thompson G.M., Kelly L.J., Candejore M.R.;  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 CC -!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.  
 DR EMBL; AF02131; AAF3407.1; --.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:005743; C:mitochondrial inner membrane; IEA.  
 DR GO; GO:005739; C:mitochondrion; IEA.  
 DR GO; GO:005488; F:binding; IEA.  
 DR GO; GO:006839; P:mitochondrial transport; IEA.  
 DR GO; GO:006810; :transport; IEA.  
 DR InterPro; IPR001993; Mitoch carrier.  
 DR IPR002030; Mit uncoupling.  
 DR Pfam; PF00153; mito\_carr; 2.  
 DR PRINTS; PR00734; MTNCOUPLING.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 2.  
 KW Membrane; Transmembrane; Transport.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ 193 AA; 20730 MW; 5DB40DB6689091DD CRC64;

Query Match 57.3%; Score 929; DB 6; Length 193;  
 Best Local Similarity 95.3%; Pred. No. 4.4e-79; Matches 183; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY |||||VKGFLGAGTAACGFDALVTPPDATAKRQLQIGENQAVQATARIVQVTRQVGLGILTMRTEGP 74  
 Db 2 |||||VKGFLGAGTAACGFDALVTPPDATAKRQLQIGENQAVQATARIVQVTRQVGLGILTMRTEGL 61  
 QY 75 CSPYNGLVAGHQROMPASTIRGLYNSVKOVYTPKGAADNSSLTRILAGCTTGAMAVTC 134  
 Db 62 CSPYNGLVAGHQROMPASTIRGLYNSVKOVYTPQADSSSLTRILAGCTTGAMAVTC 121  
 QY 135 OPTDVVKVRKRSIHLGSPRSDRKYSGTMWYRTAREEGTRGLWGTNIMRVAIVNC 194  
 Db 122 OPTDVVKVRKRSIHLGSGSDRKYSGTMWYRTAREEGTRGLWGTLPNMRAIVNC 181  
 QY 195 AEVVTVTDILKEK 206  
 Db 182 AEVVTVTDILKEK 193

Search completed: May 17, 2004, 11:52:53  
 Job time : 47 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: May 17, 2004, 11:49:15 ; Search time 17 Seconds  
(without alignments)  
955.640 Million cell updates/sec

Title: US-09-423-410-4

Perfect score: 1620

Sequence: 1 MYGLKPSDVPTMVKFLGA.....TYEQLKRALMKVQMLRBSPF 312

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched:

141681 seqB, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1620	100.0	312	UCP3_HUMAN
2	1492.5	92.1	311	UCP3_CANFIA
3	1457	89.9	308	UCP3_PIG
4	1419.5	87.5	311	UCP3_BOVIN
5	1386	85.6	308	UCP3_RAT
6	1373	84.8	308	UCP3_MOUSE
7	1165.5	71.6	309	UCP2_PIG
8	1160.5	71.4	309	UCP2_RAT
9	1156.5	71.4	309	UCP2_HUMAN
10	1149.5	71.0	309	UCP2_CANFIA
11	1145.5	70.7	309	UCP2_CYPRCA
12	1121	69.9	310	UCP2_BRABE
13	1117	69.0	310	UCP1_RABIT
14	919	56.7	306	UCP1_HUMAN
15	902.5	55.5	306	UCP1_MOUSE
16	898.5	55.5	1	UCP1_RAT
17	885.5	54.7	306	UCP1_BOVIN
18	869.5	53.7	1	UCP1_BOVIN
19	846	52.2	288	UCP5_MOUSE
20	521	32.2	1	UCP5_MOUSE
21	512	31.6	325	UCP5_HUMAN
22	475.5	29.4	323	UCP4_HUMAN
23	444	27.4	313	M20M_BOVIN
24	432	26.7	313	M20N_RAT
25	432	26.7	313	M20N_MOUSE
26	426	26.3	1	M20M_HUMAN
27	416.5	25.7	287	DIC_HUMAN
28	415.5	25.6	1	OAC1_YEAST
29	372.5	20.2	324	SFC1_YEAST
30	293	18.1	302	MCAT_MOUSE
31	273	16.9	301	MCAT_MOUSE
32	272.5	16.8	311	TXTTP_RAT
33	267	16.5	298	ADT1_BOVIN

#### ALIGNMENTS

RESULT 1
UCP3_HUMAN
ID UCP3_HUMAN STANDARD;
AC P55916; 00475; 9Q6H13;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Mitochondrial uncoupling protein 3 (UCP 3).
DE UCP3 OR SLC25A9.
GN Homo sapiens (Human), Chordata; Craniata; Vertebrata; Euteleostomi; Osteichthyes; Euteleostei; Teleostei; Actinopterygii; Sarcopterygii; Gnathostomata; Eurypterus; Euteleostomi; Bivalvia; Metzozoa; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_Taxid=9606;
OK RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=9324095; PubMed=9180264;
RA Boss O., Samec S., Paoloni-Giacobino A., Dulloo A., Seydoux J., Rossier C., Muzzin P., Giacobino J.-P., "Uncoupling protein-3: a new member of the mitochondrial carrier family with tissue-specific expression.", FEBS Lett. 408:39-42(1997).
RN RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS UCP3L AND UCP3S).
RX MEDLINE=91467312; PubMed=932552;
RA Solanes G., Vidal-Puig A., Grunig D., Flier J.S., Lowell B.B.; RT "The human uncoupling protein-3 gene. Genomic structure, chromosomal localization, and genetic basis for short and long form transcripts.", RT transcrpts.", RT J. Biol. Chem. 272:25433-25436(1997).
RT RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97150928; PubMed=9305858;
RA Gong D.-W., He Y., Karas M., Reitman M.; RT "Uncoupling protein-3 is a mediator of thermogenesis regulated by thyroid hormone, betac3-adrenergic agonists, and leptin.", RT J. Biol. Chem. 272:24129-24132(1997).
RL RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=98158426; PubMed=949861;
RA Uhhammer S.A., Dalgaard L.T., Soerensen T.I.A., Tybjaerg-Hansen A., RT "Organization of the coding exons and mutational screening of the uncoupling protein-3 gene in subjects with juvenile-onset obesity.", RT Diabetologia 41:241-244(1998).
RL RN [5]
RP SEQUENCE FROM N.A.
RX PubMed=1098796;
RA Esterbauer H., Oberkofler H., Krempeler F., Strosberg A.D., Patsch W.; RT "The uncoupling protein-3 gene is transcribed from tissue-specific promoters in humans but not in rodents.", J. Biol. Chem. 275:36394-36399(2000).
RP SEQUENCE FROM N.A. (ISOFORM 3).
RC TISSUE=Skeletal muscle;
RX MEDLINE=22388257; PubMed=12477932;



Db	241 VTKRYMSPPGOYFSPUDCMKNAQEGPTAFYKGFTPSFLRLGSNNVMVTEQLKRA	300	Qy	1 MVLGKPSDVPPTMAVKPLGACTAACFDADLVTPLDQTAKVRLQIQGENQAVOTARLVQRG	60
Qy	301 LMKVQMLRESP 312		Qy	1 MVLGKPSDVPPTMAVKPLGACTAACFDADLVTPLDQTAKVRLQIQGENQAVOTARLVQRG	60
Db	301 LMKVQMLRESP 312		Db	1 MVLGKPSDVPPTMAVKPLGACTAACFDADLVTPLDQTAKVRLQIQGENQAVOTARLVQRG	60
Qy			Qy	61 VIGTILMWRPEGESPYNGVAGLQRQMSASIRGLYKSYKVQVTPKGADNSSLTRI	120
RESULT 2			Db	61 VIGTILMWRPEGESPYNGVAGLQRQMSASIRGLYKSYKVQVTPKGADNSSLTRI	120
UCP3_CANFA			RN		
ID - UCP3_CANFA STANDARD; PRT; 311 AA.			RN		
AC 09N219; OPTS9;			RN		
DT 16-OCT-2001 (Rel. 40. Created)			RN		
DT 16-OCT-2001 (Rel. 40. Last sequence update)			RN		
DT 10-OCT-2003 (Rel. 42. Last annotation update)			RN		
DE Mitochondrial uncoupling protein 3 (UCP 3).			RN		
GN UCP3.			RN		
OS Canis familiaris (Dog).			RN		
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			RN		
OC Mammalia; Buteraria; Carnivora; Fissipedia; Canidae; Canis.			RN		
NCBI_TAXID=9615;			RN		
RA SEQIOMA FROM N.A.			RN		
RA Ishioka K.			RN		
RT "Cloning of canine UCP families.";			RN		
RL submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.			RN		
[12]			RN		
RP SEQUENCE OF 14-146 FROM N.A.			RN		
RA Thompson G.M., Kelly L.J., Candelore M.R.,			RN		
RL Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.			RN		
CC -!- FUNCTION: UCP ARE MITOCHONDRIAL TRANSPORTER PROTEINS THAT CREATE UNCOUPLING OXIDATIVE PHOSPHORYLATION AS A RESULT, ENERGY IS DISSIPATED IN THE FORM OF HEAT. MAY PLAY A ROLE IN THE MODULATION OF TISSUE RESPIRATORY CONTROL. PARTICIPATES IN THERMOGENESIS AND ENERGY BALANCE (BY SIMILARITY).			RN		
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane (By similarity).			RN		
CC -!- SIMILARITY: Belongs to the mitochondrial carrier family.			RN		
CC -!- SIMILARITY: Contains 3 Solcar repeats.			RN		
CC			RN		
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CC			RN		
CC EMBL; AB202020; BAA90458.1; -.			RN		
DR AF201378; AAP0310.1; -.			RN		
DR InterPro; IPR0030. Mit uncoupling.			RN		
DR InterPro; IPR01993; Mitoch_carrier.			RN		
DR PRINTS; PR0784; MTUCOUPLING.			RN		
DR PROSITE; PS05020; SOLCAR_3.			RN		
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.			RN		
FT TRANSMEM 11 32 1 (POTENTIAL);			RN		
FT TRANSMEM 77 99 2 (POTENTIAL);			RN		
FT TRANSMEM 120 136 3 (POTENTIAL);			RN		
FT TRANSMEM 183 199 4 (POTENTIAL);			RN		
FT TRANSMEM 217 236 5 (POTENTIAL);			RN		
FT TRANSMEM 271 293 6 (POTENTIAL).			RN		
FT REPEAT 11 105 SOLCAR_1.			RN		
FT REPEAT 114 205 SOLCAR_2.			RN		
FT DOMAIN 278 300 PURINE NUCLEOTIDE BINDING (BY SIMILARITY).			RN		
FT CONFLICT 14 14 A -> G (IN REF. 2).			RN		
FT SEQUENCE 311 AA; 34137 MW; A719FB8D6637502 CRC64;			RN		
Query Match 92.1%; Score 1492.5; DB 1; Length 311; Best Local Similarity 91.7%; Pred. No. 2.9e-129; Matches 285; Conservative 14; Mismatches 11; Indels 1; Gaps 1;			RN		
CC			RN		
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CC			RN		
CC ENBL; AF095744; AAD0881.1; -.			RN		
RESULT 3			RN		
UCP3_PIG			RN		
ID - UCP3_PIG STANDARD; PRT; 308 AA.			RN		
AC 097649; Q9XSE6;			RN		
DT 30-MAY-2000 (Rel. 39. Created)			RN		
DT 30-MAY-2000 (Rel. 39. Last sequence update)			RN		
DT 10-OCT-2003 (Rel. 42. Last annotation update)			RN		
DE Mitochondrial uncoupling protein 3 (UCP 3).			RN		
GN UCP3.			RN		
OS Sub_scorfa (Pig).			RN		
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			RN		
OC Mammalia; Buteraria; Cetartiodactyla; Suina; Suidae; Sus.			RN		
NCBI_TAXID=9823;			RN		
RA SEQUENCE FROM N.A.			RN		
RC TISSUE=White adipose tissue;			RN		
RA Werner P., Nowaczky K., Neuenschwander S., Strazinger G.;			RN		
RA "Characterization of the porcine uncoupling protein 2 and 3 (UCP2 & 3) and their localization to chromosome 9p by somatic cell hybrids.";			RN		
RL Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.			RN		
[12]			RN		
RP SEQUENCE FROM N.A.			RN		
RC STRAIN=LARGE white X Pietrain; TISSUE=Skeletal muscle;			RN		
RA Damon M., Vincent A., Herpin P.;			RN		
RA "First evidence of uncoupling protein (UCP) gene expression in piglet skeletal muscle".			RN		
RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.			RN		
CC -!- FUNCTION: UCP ARE MITOCHONDRIAL TRANSPORTER PROTEINS THAT CREATE PROTON LEAKS ACROSS THE INNER MITOCHONDRIAL MEMBRANE, THUS UNCOUPLING OXIDATIVE PHOSPHORYLATION. AS A RESULT, ENERGY IS DISSIPATED IN THE FORM OF HEAT. MAY PLAY A ROLE IN THE MODULATION OF TISSUE RESPIRATORY CONTROL. PARTICIPATES IN THERMOGENESIS AND ENERGY BALANCE (BY SIMILARITY).			RN		
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane (By similarity).			RN		
CC -!- SIMILARITY: Belongs to the mitochondrial carrier family.			RN		
CC -!- SIMILARITY: Contains 3 Solcar repeats.			RN		
CC			RN		
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CC			RN		
CC ENBL; AF095744; AAD0881.1; -.			RN		

DR EMBL; AF128837; AAD33396 1; -.  
 DR IPR002067; Mit\_CARRIER.  
 DR InterPro; IPR002030; Mit uncoupling.  
 DR Pfam; PF00153; Mitoch\_cARRIER.  
 DR PRINTS; PR00926; MITOCARRIER.  
 DR PROSITE; PS50920; SOLCAR; 3.  
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.  
 FT TRANSMEM 11 32 1 (POTENTIAL).  
 FT TRANSMEM 74 96 2 (POTENTIAL).  
 FT TRANSMEM 117 133 3 (POTENTIAL).  
 FT TRANSMEM 180 196 4 (POTENTIAL).  
 FT TRANSMEM 214 233 5 (POTENTIAL).  
 FT TRANSMEM 268 290 6 (POTENTIAL).  
 FT REPEAT 11 102 SOLCAR 1.  
 FT REPEAT 111 202 SOLCAR 2.  
 FT REPEAT 211 296 SOLCAR 3.  
 FT DOMAIN 275 297 PURINE NUCLEOTIDE BINDING (BY SIMILARITY).  
 FT CONFLICT 7 8 PS --> SD (IN REF. 2).  
 FT CONFLICT 13 13 T --> M (IN REF. 2).  
 FT CONFLICT 17 17 I --> P (IN REF. 2).  
 FT CONFLICT 49 49 A --> AVOT (IN REF. 2).  
 FT CONFLICT 150 150 R --> G (IN REF. 2).  
 SQ SEQUENCE 308 AA; 33772 MW; FDFIP2BC28FDE597 CRC64;

Query Match 89.9%; Score 1457; DB 1; Length 308;  
 Best Local Similarity 90.1%; Pred. No. 5.1e-126;  
 Matches 281; Conservative 14; Mismatches 13; Indels 4; Gaps 2;

QY 1 MYGLKSDVPMPMAKELGAGTAACTACFADLUTPLDTAKVRLQIQLGENAQAVTARLYORG 60  
 1 MYGLKSDVPMPMAKELGAGTAACTACFADLUTPLDTAKVRLQIQLGENAQAVTARLYORG 57

Dy 61 VIGTILTMVRTPGCPSPYNGVLAGLQRQMSAFASIRGLYDYSQVKVQVTPKGADNSSTRI 120  
 58 VIGTILTMVRNGPSPYNGVLAGLQRQMSAFASIRGLYDYSQVKVQVTPKGADNSSTRI 117

Db 121 LAGCTGAMAVTCQAOPDVVKVRFOAISIHLGSPSRDKYSGTMDAYRTIABEGVGLWK 180  
 118 LAGCTGAMAVTCQAOPDVVKVRFOAISIHLGSPSRDKYSGTMDAYRTIABEGVGLWK 176

Qy 181 GTPLNTRNATNCATVYTIDIKELDYLHUTDNPFCHVSAFGAGFCATVAVSPDV 240  
 177 GILPNTRNATNCATVYTIDIKELDYLHUTDNPFCHVSAFGAGFCATVAVSPDV 236

Dy 241 VTKRYMNSPPGQYFSPIDCMKVNVAQGPATYKGFTPSFLRGLGSNNVMVTVYEQLRA 300  
 237 VTKRYMNSPPGQYQNPDMKVNVTQSGPTAFYKGFTPSFLRGLGSNNVMVTVYEQLRA 296

Db 301 LMKVQMLRESPF 312  
 297 LMKVQMLRESPF 308

RESULT 4  
 UCP3\_BOVIN STANDARD; PRT; 311 AA.  
 ID \_UCP3\_BOVIN; Standard; PRT; 311 AA.  
 AC 077792; Q9TVA1; Created)  
 DT 15-JUL-1999 (Rel. 3.8, Last sequence update)  
 DT 10-OCT-2003 (Rel. 4.2, Last annotation update)  
 DE Mitochondrial uncoupling protein 3 (UCP 3).  
 GN UCP3.  
 OS Bobtaurus (Bovine).  
 OC Burkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_TAXID=9913;  
 RN [1] SEQUENCE FROM N.A.  
 RC RP TISSUE=Muscle;

RA Stone R.T., Smith T.P.L.;  
 RT "Bovine uncoupling protein 3";  
 RL Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RQ SEQUENCE OF 1-274 FROM N.A., AND VARIANT THR-53.  
 RA Stone R.T., Rexroad C.E., Smith T.P.L.;  
 RT "Bovine Ucp2 and Ucp3 map to the BTAT5.";  
 CC Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.  
 PRION PROTEIN ARB MITOCHONDRIAL TRANSPORTER PROTEINS THAT CREATE PROTON LEAKS ACROSS THE INNER MITOCHONDRIAL MEMBRANE, THUS UNCOUPLING OXIDATIVE PHOSPHORYLATION. AS A RESULT, ENERGY IS DISSIPATED IN THE FORM OF HEAT. MAY PLAY A ROLE IN THE MODULATION OF TISSUE RESPIRATORY CONTROL. PARTICIPATES IN THERMOGENESIS AND ENERGY BALANCE (BY SIMILARITY).  
 CC SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane (By similarity).  
 CC -!- SIMILARITY: Belongs to the mitochondrial carrier family.  
 CC -!- SIMILARITY: Contains 3 Solcar repeats.  
 CC -----  
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 CC -----  
 DR EMBL; AF092048; AAC61762\_1; -.  
 DR InterPro; IPR002030; Mit\_uncoupling.  
 DR IPR002067; Mit\_cARRIER.  
 DR Pfam; PF00153; mito\_Carr; 3.  
 DR PRINTS; PR00926; MITOCARRIER.  
 DR PROSITE; PS50920; SOLCAR; 3.  
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.  
 FT TRANSMEM 11 32 1 (POTENTIAL).  
 FT TRANSMEM 77 99 2 (POTENTIAL).  
 FT TRANSMEM 120 136 3 (POTENTIAL).  
 FT TRANSMEM 183 199 4 (POTENTIAL).  
 FT TRANSMEM 217 236 5 (POTENTIAL).  
 FT TRANSMEM 217 293 6 (POTENTIAL).  
 FT REPEAT 11 105 SOLCAR 1.  
 FT REPEAT 114 205 SOLCAR 2.  
 FT REPEAT 214 299 SOLCAR 3.  
 FT DOMAIN 278 300 PURINE NUCLEOTIDE BINDING (BY SIMILARITY).  
 FT VARIANT 53 53 A --> T.  
 SQ SEQUENCE 311 AA; 34205 MW; BIAD2625650D04 CRC64;

Query Match 87.6%; Score 1419.5; DB 1; Length 311;  
 Best Local Similarity 87.2%; Pred. No. 1.4e-122;  
 Matches 272; Conservative 17; Mismatches 22; Indels 1; Gaps 1;

Qy 1 MYGLKSDVPMPMAKELGAGTAACTACFADLUTPLDTAKVRLQIQLGENAQAVTARLYORG 60  
 1 MYGLKSDVPMPMAKELGAGTAACTACFADLUTPLDTAKVRLQIQLGENAQAVTARLYORG 60

Dy 61 VIGTILTMVRNGPSPYNGVLAGLQRQMSAFASIRGLYDYSQVKVQVTPKGADNSSTRI 120  
 61 VIGTILTMVRNGPSPYNGVLAGLQRQMSAFASIRGLYDYSQVKVQVTPKGADNSSTRI 120

Qy 121 LAGCTGAMAVTCQAOPDVVKVRFOAISIHLGSPSRDKYSGTMDAYRTIABEGVGLWK 180  
 121 LAGCTGAMAVTCQAOPDVVKVRFOAISIHLGSPSRDKYSGTMDAYRTIABEGVGLWK 179

Dy 121 LAGCTGAMAVTCQAOPDVVKVRFOAISIHLGSPSRDKYSGTMDAYRTIABEGVGLWK 179  
 181 GTPLNTRNATNCATVYTIDIKELDYLHUTDNPFCHVSAFGAGFCATVAVSPDV 240  
 180 GILPNTRNATNCATVYTIDIKELDYLHUTDNPFCHVSAFGAGFCATVAVSPDV 239

Qy 241 VTKRYMNSPPGQYFSPIDCMKVNVAQGPATYKGFTPSFLRGLGSNNVMVTVYEQLRA 300

**RESULT 5**

Db 240 VTKRYVNSPCCQYHSPFDCMLKMKVYQEGPTAFYKGTPSFRLGSWNVMVWVYBQMRA 299  
 ID UCP3\_RAT STANDARD; PRT; 308 AA.  
 AC P56479; 15-JUL-1998 (Rel. 36, Created)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Mitochondrial uncoupling protein 3 (UCP 3).  
 GN UCP3  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TAXID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Skeletal muscle;  
 RX MEDLINE=91074937; PubMed=941426;  
 RA Matsuda J., Horoda K., Ichijo H., Son C., Doi K., Tanaka T.,  
 RA Fukunaga Y., Inoue G., Nishimura H., Yoshimae Y., Yamori Y.,  
 RA Nakao K.;  
 RT "Cloning of rat uncoupling protein-3 and uncoupling protein-2 cDNAs: their gene expression in rats fed high-fat diet.", FEBS Lett. 418:200-204(1997).  
 RL [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=Wisbar; TISSUE=Skeletal muscle;  
 RX MEDLINE=93165302; PubMed=9506477;  
 RA O., Samec S., Desplanches D., Mayet M.-H., Seydoux J., Muzzin P., Giacobino J.-P.;  
 RT "Effect of endurance training on mRNA expression of uncoupling proteins 1, 2, and 3 in the rat.", J. Physiol. 511:335-339(1998).  
 RL [3]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Skeletal muscle;  
 RX MEDLINE=98400868; PubMed=9725803;  
 RA Lin B.-Z., Coughlin S., Pilch P.F.;  
 RT "Bidirectional regulation of uncoupling protein-3 and GLUT-4 mRNA in skeletal muscle by cold.", Am. J. Physiol. 275:E386-E391(1998).  
 RL [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Skeletal muscle;  
 RA Solanas G., Valet P., Lowell B.B.;  
 RT "Lipo polysaccharide treatment increases thermogenesis and induces uncoupling protein-3 gene expression in skeletal muscle.", submitted (Oct-1997) to the EMBL/GenBank/DDBJ databases.  
 RL PROTON LEAKS ACROSS THE INNER MITOCHONDRIAL MEMBRANE THAT CREATE UNCOUPLING OXIDATIVE PHOSPHORYLATION. AS A RESULT, ENERGY IS DISSIPATED IN THE FORM OF HEAT. MAY PLAY A ROLE IN THE MODULATION OF TISSUE RESPIRATORY CONTROL. PARTICIPATES IN THERMOGENESIS AND ENERGY BALANCE (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: Intermembrane protein, Mitochondrial inner membrane (By similarity)  
 CC -!- SIMILARITY: Belongs to the mitochondrial carrier family.  
 CC -!- SIMILARITY: Contains 3 Solute repeats.  
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**RESULT 6**

Db 301 LMKVQMLRESPF 312  
 ID UCP3\_MOUSE STANDARD; PRT; 308 AA.  
 AC P56501; 08/29/3; 15-JUL-1998 (Rel. 36, Created)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Mitochondrial uncoupling protein 3 (UCP 3).  
 GN UCP3  
 OS Mus musculus (Mouse).  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TAXID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RC Sanchis D., Fleury C., Bouillaud F., Ricquier D.;  
 RL Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.

RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Swiss Webster; TISSUE=Embryo;  
 RX MEDLINE=98332721; PubMed=966083;  
 RA Yoshiomi H., Yamazaki K., Tanaka I.;  
 RT "Cloning of mouse uncoupling protein 3 cDNA and 5'-flanking region,  
 and its genetic map.";  
 RL Gene 215:77-84 (1998).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c; TISSUE=Skeletal muscle;  
 RA Grujic D., Zhan C.-Y., Sleicher L.J., Lowell B.B.;  
 RT Submitted (OCT-1997) to the EMBL/GenBank/DDJB databases.  
 RL [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=OTBL/6J; TISSUE=Skeletal muscle;  
 RA Son C., Hosoda K., Matsuda J., Nakao K.;  
 RT "Cloning of mouse UCP3 cDNA."  
 RL Submitted (OCT-1997) to the EMBL/GenBank/DDJB databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9916732; PubMed=10066417;  
 RA Gong D.W., He Y., Reitman M.L.;  
 RT "Genomic organization and regulation by dietary fat of the uncoupling  
 protein 3 and 2 genes.";  
 RL Biochem. Biophys. Res. Commun. 256:27-32(1999).  
 RN [6]  
 RP SEQUENCE OF 84-180 FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Skeletal muscle;  
 RX MEDLINE=98262557; PubMed=960008;  
 RA Shimokawa T., Kato M., Ezaki O., Hashimoto S.;  
 RT "Transcriptional regulation of muscle-specific genes during myoblast  
 differentiation.";  
 RL Biochem. Biophys. Res. Commun. 246:287-292(1998).  
 RN [7]  
 RP SEQUENCE OF 162-252 FROM N.A.  
 RA Yan X., Ramsay T.G.;  
 RL Submitted (OCT-1997) to the EMBL/GenBank/DDJB databases.  
 CC FUNCTION: UCP ARE MITOCHONDRIAL TRANSPORTER PROTEINS THAT CREATE  
 PROTON LEAKS ACROSS THE INNER MITOCHONDRIAL MEMBRANE, THUS  
 UNCOUPLING OXIDATIVE PHOSPHORYLATION AS A RESULT ENERGY IS  
 DISSIPATED IN THE FORM OF HEAT. MAY PLAY A ROLE IN THE MODULATION  
 OF TISSUE RESPIRATORY CONTROL. PARTICIPATES IN THERMOGENESIS AND  
 ENERGY BALANCE(BY SIMILARITY).  
 CC SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 inner membrane (By similarity).  
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
 CC -1- SIMILARITY: Contains 3 Soscar repeats.  
 CC  
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 or send an email to [license@ebi-sib.ch](mailto:license@ebi-sib.ch)).  
 -----  
 DR PRINTS: PR00926; MITOCARRIER.  
 DR PRINTS; PR00784; MTUNCOPPLING.  
 DR PROSITE; PS50920; SOLCAR; 3.  
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.  
 PT TRANSMEM 11 32 1 (POTENTIAL).  
 PT TRANSMEM 74 96 2 (POTENTIAL).  
 PT TRANSMEM 117 133 3 (POTENTIAL).  
 PT TRANSMEM 180 196 4 (POTENTIAL).  
 PT TRANSMEM 214 233 5 (POTENTIAL).  
 PT TRANSMEM 268 290 6 (POTENTIAL).  
 PT REPEAT 11 102 SOLCAR 1.  
 PT REPEAT 111 202 SOLCAR 2.  
 PT REPEAT 211 296 SOLCAR 3.  
 FT DOMAIN 275 297 PURINE NUCLEOTIDE BINDING (BY  
 SIMILARITY).  
 FT CONFLICT 179 179 W -> L (IN REF. 6).  
 FT SEQUENCE 308 AA; 33910 MW; 12CAD674DFD0C3 CRC64;  
 DR  
 Query Match 84.8%; Score 313; DB 1; Length 308;  
 Best Local Similarity 85.6%; Pred. No. 2.5e-18; Mismatches 23; Indels 4; Gaps 2;  
 Matches 267; Conservative 18; Mismatches 23; Indels 4; Gaps 2;  
 DR  
 Qy 1 MVGLKPSPDPPTMAVKPKEGAGTAACFAPDVTPEPDATKYLQLOQENGDVAVTARIWQRC 60  
 Db 1 MVGLKPSPDPPTMAVKPKEGAGTAACFAPDVTPEPDATKYLQLOQENGDVAVTARIWQRC 57  
 Qy 61 VLGILTMMTRTEGGCSPSPNCLVAGIQLQRQMSFASPRIGYDYSVKQVTPKGADNLSTIRI 120  
 Db 58 VLGLTLMTRTEGGCSPSPNCLVAGIQLQRQMSFASPRIGYDYSVKQVTPKGADNLSTIRI 117  
 DR  
 Qy 121 LAGCTTGAMVTCOPTDVKVRQASLNGPSASDRKISGTMAYRTAREVGKMK 180  
 Db 118 LAGCTTGAMVTCOPTDVKVRQASLNGPSASDRKISGTMAYRTAREVGKMK 176  
 DR  
 Qy 181 GTLPNIMMRNAIVNGAEVRYDILGEKLUDYHLLTDNPFRCPHFVSARGAGFCATVAVSPUDV 240  
 Db 177 GIWPNTNTRALVNCAEMTVDTIKERKLISHLTFDNPFCHFVSARGAGFCATVAVSPUDV 236  
 DR  
 Qy 241 VKTRTPNSPPGQYSPSPUDCMIKMVAQEGPAPYGFSPRLIGSWNWNVMTVEQLRA 300  
 Db 237 VKTRTPNSPPGQYSPSPUDCMIKMVAQEGPAPYGFSPRLIGSWNWNVMTVEQLRA 296  
 DR  
 Qy 301 LMKVQMLRESPF 312  
 Db 297 LMKVQMLRESPF 308  
 DR  
 RESULT 7  
 UCP2\_MOUSE STANDARD; PRT; 309 AA.  
 DR ID P70456; O88285;  
 DT 01-Nov-1997 (Rel. 35, Created)  
 DT 01-Nov-1997 (Rel. 35, last sequence update)  
 DT 15-Mar-2004 (Rel. 43, last annotation update)  
 DR Mitochondrial uncoupling protein 2 (UCP2) (UCP2).  
 DR Mitochondrial uncoupling protein 2 (UCP2).  
 DR  
 OS Mus musculus (Mouse).  
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus.  
 DR NCBI\_TaxID=10090;  
 DR  
 RN 1  
 DR SEQUENCE FROM N.A.  
 DR STRAIN=BALB/c; TISSUE=Muscle;  
 DR Rainbaud S., Bouillaud F., Ricquier D.;  
 DR Submitted (SEP-1996) to the EMBL/GenBank/DDJB databases.  
 DR  
 RN 2  
 DR SEQUENCE FROM N.A.  
 DR TISSUE=Spleen;  
 DR MEDLINE=97278985; PubMed=9133562;  
 DR Ginev R.E., Dembski M., Weng X., Deng N., Shyjan A.W.,  
 DR Gimeno C.J., Iris F., Ellis S.J., Wolf B.A., Tartaglia L.A.;  
 DR InterPro; IPR002303; Mit uncoupling.  
 DR InterPro; IPR01993; Mitoch\_carrier.  
 DR Pfam; PF00153; mito\_carr; 3.





Query Match 71.4%; Score 1156.5; DB 1; Length 309;  
 Best Local Similarity 72.2%; Pred. No. 1.7e-98; Mismatches 50; Indels 5; Gaps 3;

**Matches 226; Conservative 32; Mismatches 50; Indels 5; Gaps 3;**

**Qy** 1 MYGLKSKSDVPPMVKFLGAGTACRFLDLYPFLDKVRLQKIQGNOAV-CATARLVOYR 59  
**Db** 1 MYGPKAKADVPPATKFLGAGTACRFLDLYPFLDKVRLQKIQGNOAV-CATARLVOYR 59  
**Qy** 60 GUIGLTILTMVRTEGPGCSPYNGVJAGLORMSASIRGLYNSVKQVTPKADNSSLTR 119  
**Db** 61 GUIGLTILTMVRTEGPGCSPYNGVJAGLORMSASIRGLYNSVKQVTPKADNSSLTR 119  
**Qy** 120 ILAGCTTGAMAVTCAGAOPDVVKVFOAISIHLGSPSRSDRKYSTMDAVRTARBEBURGLW 179  
**Db** 120 LIAGSTGALAVAVQAQTDVKVRFQOARAG--GARRYQSTIVEAVKTIAREGRLW 176  
**Qy** 180 KCTLPNPNRNAUNCAASVVTYILKEKULDMHLLDNPCHVSARGAFCTVVASPD 239  
**Db** 177 KGPSPNVARNAUNCTELVYDILKOTIKANLMIDPLCPHTSAFFAGFCITVASPD 236  
**Qy** 240 VVKTIVMSPPQYFSPLDCKMKAQVAGPTFVKGTPSERLGSNNVWVMTYSLKR 299  
**Db** 237 VVKTIVMSPPQYHSAHGCAJLWRKREGPRAFKGFMPSFLRLGSNNVWVMTYSLKR 296  
**Qy** 300 ALMKVQMLRESP 312  
**Db** 297 ALMAYAESREAPP 309

**RESULT 10**

**UCP2\_HUMAN STANDARD; PRT; 309 AA.**

**ID UCP2\_HUMAN STANDARD; PRT; 309 AA.**

**AC P55851; 01-NOV-1997 (Rel. 35, Created)**  
**DT 01-NOV-1997 (Rel. 35, Last sequence update)**  
**DT 2001-OCT-2003 (Rel. 42, Last annotation update)**  
**DE Mitochondrial uncoupling protein 2 (UCP2) (UCPH).**  
**GN UCP2 OR SLC25A8.**

**OS Homo sapiens (Human).**

**OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.**

**OC NCBI\_TaxID:9606;**  
**RN [1]**  
**RP SBQUENCE FROM N.A.**

**RC TISSUE=Skeletal muscle;**  
**RX MEDLINE=97224095; PubMed=9180264;**  
**RX Boss O., Sanez S., Proloni-Giacobino A., Dulloo A., Seydoux J., Rosier C., Muzzin P., Giacobino J.-P.;**  
**RT "Uncopling protein-3: a new member of the mitochondrial carrier family within tissue-specific expression.";**  
**RL FEBS Lett. 408:39-42(1997).**  
**RN [2]**  
**RP SBQUENCE FROM N.A.**

**RC TISSUE=Lung, and Skeletal muscle;**  
**RX MEDLINE=97207646; PubMed=9054939;**  
**RX Fleury C., Neverova M., Collins S., Rainbault S., Champigny O., Levi-Meyrueis C., Bonillaud F., Seldin M.F., Surwit R.S., Ricquier D., Warden C.H.;**  
**RT "uncoupling protein-2: a novel gene linked to obesity and diabetes";**  
**RT Diabetees 46:900-906 (1997).**  
**RN [4]**  
**RP SEQUENCE FROM N.A., AND VARIANT VAL-55.**

**RA Klannemark M., Orho M., Groop L.; Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.**

**RK [5]**  
**RE SEQUENCE FROM N.A.**

**RX MEDLINE=98227655; PubMed=9568704;**  
**RX Argyropoulos G., Brown A.M., Peterson R., Likes C.E., Watson D.K., Garvey W.T.;**  
**RT "Structure and organization of the human uncoupling protein 2 gene and identification of a common biallelic variant in Caucasian and African-American subjects.,";**  
**RT Diabetes 47:685-687(1998).**  
**RK [6]**  
**RN SEQUENCE FROM N.A.**

**RC TISSUE=Placenta;**  
**RX MEDLINE=99185293; PubMed=10082652;**  
**RX Pequignot G., Cassard-Doulcier A.M., Rainbault S., Miroux B., Fleury C., Gelly C., Bouillaud F., Ricquier D., Bhat N.K.,**  
**"Functional organization of the human uncoupling protein-2 gene, and juxtaposition to the uncoupling protein-3 gene.,";**  
**RT Biochem. Biophys. Res. Commun. 255:40-46(1999).**  
**RK [7]**  
**RN SEQUENCE FROM N.A.**

**RC TISSUE=B-cell;**  
**RX MEDLINE=22388257; PubMed=12477932;**  
**RX Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schatz T.E., Brownstein M.J., Usdin T.B., Toshiraku S., Corninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muany D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahay J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Blakeley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.N., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E., Schnerch A., Schein J.E., Jones S.J.M., Marr M.A.,**  
**RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.,";**  
**RK PROC. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).**  
**CC -I- FUNCTION: UCP are mitochondrial transporter proteins that create proton leaks across the inner mitochondrial membrane, thus uncoupling oxidative phosphorylation from ATP synthesis. As a result, energy is dissipated in the form of heat.**  
**CC -I- SUBUNIT: Acts as a dimer forming a proton channel (By similarity).**  
**CC -I- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.**  
**CC -I- TISSUE SPECIFICITY: Widely expressed in adult human tissues, including tissues rich in macrophages. Most expressed in white adipose tissue and skeletal muscle.**  
**CC -I- SIMILARITY: Belongs to the mitochondrial carrier family.**  
**CC -I- SIMILARITY: Contains 3 Solcat repeats.**

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**CC EMBL; U82819; AAC51336.1; -;**  
**DR EMBL; U94592; AAB53091.1; -;**  
**DR EMBL; AU223477; CRA1402.1; -;**  
**DR EMBL; AU223478; CRA1402.1; JOINED.**  
**DR EMBL; AU223479; CAA11402.1; JOINED.**  
**DR EMBL; AF019401; AAC29690.1; -;**  
**DR EMBL; AF096289; RAD21151.1; -;**

DR EMBL; BC011737; AAH11737.1; -.

DR DR Genev; HGNC;12518; UCP2.

DR DR GO; GO:0015633; F: uncoupling Protein activity; TAS.

DR DR GO; GO:0015992; P: proton transport; TAS.

DR InterPro; IPR002030; Mit uncoupling.

DR InterPro; IPR011993; mito\_carr\_3.

DR PRIMs; PR00784; MTCOUPLING.

DR PROSITE; PS50920; SOLCAR; 3.

KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport; KW Polymorphism.

FT TRANSMEM 11 32 1 (POTENTIAL).

FT TRANSMEM 78 100 2 (POTENTIAL).

FT TRANSMEM 120 136 3 (POTENTIAL).

FT TRANSMEM 181 197 4 (POTENTIAL).

FT TRANSMEM 215 234 5 (POTENTIAL).

FT TRANSMEM 269 291 6 (POTENTIAL).

FT REPEAT 11 106 SOLCAR 1.

FT REPEAT 114 203 SOLCAR 2.

FT REPEAT 212 297 SOLCAR 3.

FT DOMAIN 276 298 PURINE NUCLEOTIDE BINDING (BY SIMILARITY).

FT VARIANT 55 55 A -> V (in dbSNP:660339).

FT CONFLICT 219 219 /FTID=VAR016129; T -> I (IN REF. 2).

SQ SEQUENCE 309 AA; 33229 MW; 2E174139162183D9 CRC64;

Query Match Best Local Similarity 72.2%; Pred. No. 7.6e-98; Matches 226; Conservative 31; Mismatches 51; Indels 5; Gaps 3; Score 1149.5; DB 1; Length 309;

QY 1 MGLKLSDVPPMMAVKELGAGTAACFADLIVPLDVTAKVRLQI0GENQA-VOTARLWQYR 59

Db 1 MVGPKATDVPPATVKFLGAGTAACFADLITPLDTAKVRLQI0GENQA-VOTARLWQYR 60

QY 60 GVLGTILTMVRTEGPSPSYNGLVAGLQRQMSPASTRIGLYSVKQVTPKAGDNSSLTR 119

Db 61 GVGTLTILMVTEGPSPSYNGLVAGLQRQMSPASTRIGLYSVKQVTPKAGDNSSLTR 119

QY 120 ILAGCTTGAMAVTCAPTDVKURFOASIHGSPRSRDKYSGTMDAIRTARBEGYGLW 179

Db 120 ILAGSTTGALAVAVQDPDVKTFQOARG--SGRRYKSTVDVKTARBEERGLW 176

QY 180 KGTLPNMRNATVCAEVWYDILKEKLLDYLHNTNPFCHVSARGAFCATVVASPVD 239

Db 177 KGTSPNMRNATVCAEVWYDILKEKLLDYLHNTNPFCHVSARGAFCATVVASPVD 236

QY 240 VKTRYMSPPQYFSLDCKMKVQAQGPFAFKGTFPSLRLGSWNVMFTYSLKR 299

Db 237 VKTRYMSALQGQSSAGCHALTMLQEGPRAFYKGMPSPFLRLGSWNVMFTYSLKR 296

QY 300 ALMKVOMLRESPF 312

Db 297 ALMAACTSREAPP 309

RESULT 11

UCP2\_CANFA ID: CANFA STANDARD; PRT; 309 AA.

AC Q9N2J1; Q9RTTO; 16-OCT-2001 (Rel. 40, Created)

AC Q9N2J1; Q9RTTO; 16-OCT-2001 (Rel. 40, Last sequence update)

AC Q9N2J1; Q9RTTO; 16-OCT-2003 (Rel. 42, Last annotation update)

DE Mitochondrial uncoupling protein 2 (UCP-2).

GN UCP2.

OS Canis familiaris (Dog)

OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Etheria; Carnivora; Fissipedia; Canidae; Canis.

RN [1]

RP SEQUENCE FROM N.A.

RA Ibioka K.;

RQ "Cloning of canine UCP families." Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.

RQ [2]

RQ SEQUENCE OF 4-197 FROM N.A.

RQ RA Thompson G.M., Kelly L.J., Candeiro M.R.; Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

RQ CC CTC -!- FUNCTION: UCP are mitochondrial transporter proteins that create proton leaks across the inner mitochondrial membrane, thus uncoupling oxidative phosphorylation from ATP synthesis. As a result, energy is dissipated in the form of heat (By similarity).

RQ CC CTC -!- SUBUNIT: Acts as a dimer forming a proton channel (By similarity).

RQ CC CTC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.

RQ CC CTC -!- SIMILARITY: Belongs to the mitochondrial carrier family.

RQ CC CTC -!- SIMILARITY: Contains 3 Solcar repeats.

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RQ CC CTC EMBL; AB020887; BA90457.1; EMBL; AF201377; AA08309.1; -.

RQ CC CTC DR InterPro; IPR002030; Mit uncoupling.

RQ CC CTC DR InterPro; IPR0011993; Mito\_carr.

RQ CC CTC DR PRIMs; PR00153; mito\_carr\_3.

RQ CC CTC DR PROSITE; PR00784; MTCOUPLING.

RQ CC CTC DR PS50920; SOLCAR; 3.

RQ CC CTC KW Mitochondrion; Transmembrane; Transport; Repeat.

RQ CC CTC FT TRANSMEM 11 32 1 (POTENTIAL).

RQ CC CTC FT TRANSMEM 78 100 2 (POTENTIAL).

RQ CC CTC FT TRANSMEM 120 136 3 (POTENTIAL).

RQ CC CTC FT TRANSMEM 181 197 4 (POTENTIAL).

RQ CC CTC FT TRANSMEM 215 234 5 (POTENTIAL).

RQ CC CTC FT TRANSMEM 269 291 6 (POTENTIAL).

RQ CC CTC FT REPEAT 11 106 SOLCAR 1.

RQ CC CTC FT REPEAT 114 203 SOLCAR 2.

RQ CC CTC FT DOMAIN 276 298 PURINE NUCLEOTIDE BINDING (BY SIMILARITY).

RQ CC CTC FT CONFLICT 64 64 C -> G (IN REF. 2).

RQ CC CTC SQ SEQUENCE 309 AA; 33270 MW; D9860F0E8B870BF CRC64;

Query Match Best Local Similarity 72.5%; Pred. No. 1.8e-97; Matches 227; Conservative 29; Mismatches 52; Indels 5; Gaps 3; Score 1145.5; DB 1; Length 309;

QY 1 MGLKLSDVPPMMAVKELGAGTAACFADLIVPLDVTAKVRLQI0GENQA-VOTARLWQYR 59

Db 1 MVGPKATDVPPATVKFLGAGTAACFADLITPLDTAKVRLQI0GENQA-VOTARLWQYR 60

QY 60 GVLGTILTMVRTEGPSPSYNGLVAGLQRQMSPASTRIGLYSVKQVTPKAGDNSSLTR 119

Db 61 GVGTLTILMVTEGPSPSYNGLVAGLQRQMSPASTRIGLYSVKQVTPKAGDNSSLTR 119

QY 120 ILAGCTTGAMAVTCAPTDVKURFOASIHGSPRSRDKYSGTMDAIRTARBEGYGLW 179

Db 177 KGTSPNMRNATVCAEVWYDILKEKLLDYLHNTNPFCHVSARGAFCATVVASPVD 236

QY 240 VKTRYMSPPQYFSLDCKMKVQAQGPFAFKGTFPSLRLGSWNVMFTYSLKR 299

Db 237 VKTRYMSALQGQSSAGCHALTMLQEGPRAFYKGMPSPFLRLGSWNVMFTYSLKR 296

QY 300 ALMKVOMLRESPF 312

Db 297 ALMAACTSREAPP 309

RESULT 12  
 UCP2\_CYPCA STANDARD PRT; 310 AA.  
 ID UCP2\_CYPCA STANDARD PRT; 310 AA.  
 AC Q9W725; 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DB Mitochondrial uncoupling protein 2 (UCP 2).  
 GN UCP2.  
 OS Cyprinus carpio (Common carp).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Cyprinidae.  
 OX NCBI\_TaxID=7962;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Stuart J.A., Harper J.A., Brindle K.M., Brand M.D.; UCP2 from cold-blooded vertebrates., to the EMBL/GenBank/DDJB databases.  
 RT Submitted (JUN-1999) ;  
 CC -!- FUNCTION: UCP are mitochondrial transporter proteins that create proton leaks across the inner mitochondrial membrane, thus uncoupling oxidative phosphorylation from ATP synthesis. As a result, energy is dissipated in the form of heat (By similarity).  
 CC -!- SUBUNIT: Acts as a dimer forming a proton channel (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.  
 CC -!- SIMILARITY: Belongs to the mitochondrial carrier family.  
 CC -!- SIMILARITY: Contains 3 Solcar repeats.  
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 CC EMBL: AJ43486; CAB6248 1; -  
 DR InterPro; IPR002030; Mit\_uncoupling.  
 DR PF00153; mito\_carr; 3;  
 DR PRINTS; PRO0784; MITUNCOPPLING.  
 DR PROSITE; PS50920; SOLCAR; 3.  
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.  
 FT TRANSMEM 11 32 1 (POTENTIAL).  
 FT TRANSMEM 79 101 2 (POTENTIAL).  
 FT TRANSMEM 121 137 3 (POTENTIAL).  
 FT TRANSMEM 182 198 4 (POTENTIAL).  
 FT TRANSMEM 216 235 5 (POTENTIAL).  
 FT TRANSMEM 270 292 6 (POTENTIAL).  
 FT REPEAT 11 107 SOLCAR 1.  
 FT REPEAT 115 204 SOLCAR 2.  
 FT REPEAT 213 298 SOLCAR 3.  
 FT DOMAIN 277 299 PURINE NUCLEOTIDE BINDING (BY SEQUENCE 310 AA; 33532 MW; AD0EAD733C73704E CRC64; Query Match 69.2%; Score 1121; DB 1; Length 310; Best Local Similarity 72.4%; Pred. No. 3.1e-35; Matches 220; Conservative 31; Mismatches 47; Indels 6; Gaps 4;

RESULT 13  
 UCP2\_BRARE STANDARD PRT; 310 AA.  
 ID UCP2\_BRARE STANDARD PRT; 310 AA.  
 AC Q9W720; 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DB Mitochondrial uncoupling protein 2 (UCP 2).  
 ON UCP2.  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Stuart J.A., Harper J.A., Brindle K.M., Brand M.D.; UCPs from cold-blooded vertebrates., to the EMBL/GenBank/DDJB databases.  
 RT Submitted (JUN-1999) ;  
 CC -!- FUNCTION: UCP are mitochondrial transporter proteins that create proton leaks across the inner mitochondrial membrane, thus uncoupling oxidative phosphorylation from ATP synthesis. As a result, energy is dissipated in the form of heat (By similarity).  
 CC -!- SUBUNIT: Acts as a dimer forming a proton channel (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.  
 CC -!- SIMILARITY: Belongs to the mitochondrial carrier family.  
 CC -!- SIMILARITY: Contains 3 Solcar repeats.  
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 CC EMBL: AJ43250; CAB6268 1; -  
 DR ZFIN; ZDB-GENE-990708-8; ucp2.  
 DR InterPro; IPR002030; Mit uncoupling.  
 DR InterPro; IPR001993; Mitoch\_carrier.  
 DR Pfam; PF00153; mito\_carr; 3;  
 DR PRINTS; PRO0784; MITUNCOPPLING.  
 DR PROSITE; PS50920; SOLCAR; 3.  
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.  
 FT TRANSMEM 11 32 1 (POTENTIAL).  
 FT TRANSMEM 79 101 2 (POTENTIAL).  
 FT TRANSMEM 121 137 3 (POTENTIAL).  
 FT TRANSMEM 182 198 4 (POTENTIAL).  
 FT TRANSMEM 216 235 5 (POTENTIAL).  
 FT TRANSMEM 270 292 6 (POTENTIAL).  
 FT REPEAT 11 107 SOLCAR 1.  
 FT REPEAT 115 204 SOLCAR 2.  
 FT DOMAIN 277 299 PURINE NUCLEOTIDE BINDING (BY SIMILARITY).

FT 59 RCGVLTGTTMPTTTEGCPSPYVLSVQHOMFASTIRIGLYNSVKVQYTPKCADNLSLT 118  
 Db 1 MGPRGDGVPPRATVKIGPACIADLFPFLDKVRIQDGSKIPNTGHPVY 60  
 Qy 61 RGVFGTISTMVREVGPSLVSYSVQHOMFAASVRLGIVYDSVKQFYT-KSEEHVGIGS 119  
 Qy 119 RLAGCTTGAMVTCAGPTDVVKVRQASIHGSPSISDRKSYSGTMAYRTAAREGVGL 178



Db 236 VKTRFINSPPGQYKSVNPMKVFTEQPTAFFKGIVPSFLRGSMNVIMFVCFEQLRE 295  
Qy 301 LMK 303  
Db 296 LSK 298

Search completed: May 17, 2004, 11:53:22  
Job time: 18 secs

RA Bouillaud F.; Ricquier D.; Raimbault S.;  
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.  
 CC -!- PROJECTION: UCP are mitochondrial transporter proteins that create  
 CC proton leaks across the inner mitochondrial membrane, thus  
 CC uncoupling oxidative phosphorylation from ATP synthesis. As a  
 result, energy is dissipated in the form of heat.  
 CC -!- SUBUNIT: Acts as a dimer forming a proton channel.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -!- TISSUE SPECIFICITY: Brown adipose tissue.  
 CC -!- SIMILARITY: Belongs to the mitochondrial carrier family.  
 CC -!- SIMILARITY: Contains 3 Solcar repeats.  
 CC  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC  
 DR EMBL; X51952; CAA36214.1; -.  
 DR EMBL; X51953; CAA36214.1; JOINED.  
 DR EMBL; X51954; CAA36214.1; JOINED.  
 DR EMBL; X51955; CAA36214.1; JOINED.  
 DR EMBL; U28480; AAB85271.1; -.  
 DR PIR; GO1858; G01858.  
 DR GeneID; HGNC:12517; UCPI.  
 DR MIM; 113730; -.  
 DR GO; GO-0015892; P-proton transport; TAS.  
 DR Interpro; IPR002030; Mitt\_uncoupling.  
 DR Interpro; IPR01933; Mito\_carr; 3.  
 DR PFAM; PPF00153; mltcarr; 3.  
 DR PRINTS; PRO0074; MRUNCOPPLING.  
 DR PROSITE; PS00920; SOLCAR; 3.  
 KW Mitochondrion, inner membrane; Repeat; Transmembrane; Transport.  
 FT TRANSMEM 11 32 1 (POTENTIAL).  
 FT TRANSMEM 74 96 2 (POTENTIAL).  
 FT TRANSMEM 117 133 3 (POTENTIAL).  
 FT TRANSMEM 179 195 4 (POTENTIAL).  
 FT TRANSMEM 213 232 5 (POTENTIAL).  
 FT TRANSMEM 277 289 6 (POTENTIAL).  
 FT REPEAT 11 102 SOLCAR 1.  
 FT REPEAT 111 201 SOLCAR 2.  
 FT REPEAT 210 295 SOLCAR 3.  
 FT DOMAIN 274 296 PURINE NUCLEOTIDE BINDING  
 FT CONFLICT 21 21 (BY SIMILARITY).  
 SQ SEQUENCE 307 AA; 33044 MW; 341BC7F0155AF9B4 CRC64;  
 Query Match 55 7%; Score 902.5; DB 1; Length 307;  
 Best Local Similarity 58.4%; Pred. No. 3.2e-75; Mismatches  
 Matches 177; Conservative 47; Mismatches 74; Indels 5; Gaps 2  
 QY 1 MVGIKPSDPVPTMAVKFLGACTAAFPADLVTPPLDTAKVRLQIQLQGENAQAVTARLWQRG 60  
 QY 1 MGGSITASDHPHTPLGVQLQFSAPIAATLADLADIVTPPLDTAKVRLQVOGE--CPTSS VRYKG 57  
 QY 61 VLGLTILTMWTEPGCPSPYNGILAGIQRMSTASIRIGLYDYSVQKVYPKGADNSSLTRI 120  
 QY 58 VLGITITAVKIEGRMKVLYSSLPAGLQRQISSASLRIGLYDVTQEFULTAGKETAPSLSKSI 117  
 Db 181 GTLPLNMIRMAVNCALAEVYTDILKEKULDYLITDNEPCHVTSAGFGFCATWVASPV 240  
 Qy 121 LAGCTTGAMAVTCAPTDVVKYRFQASHGSPRSRDKYSGTMADYTARREBVRGSIWK 180  
 Db 176 GTTENLMLRSVIINCTELVUTDLMKAEFKVNLLDADVPCHLVSLAIIAGCATAMSSPV 235  
 Db 118 LAGLTGGVAVFIGOPTEVVKVLQAOQSHLHGKPP--RTYGTYNMARIATTEGTLGLW 175  
 QY 241 VKTRVMNSPQQYFFPLDCMKVNAQOBGPMTFYKGTSPFLRLGSWAVMFYBQJKRA 3000